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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:24:34 ; Search time 114.5 seconds  
(without alignments)  
23,936 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186  
Sequence: 1 MLKLKGDIDSNAAIDLSNKASLAFLOKHLGKHFQ 37

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

- 1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.\*
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- 8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	100.0	441	21	Human low density
2	186	100.0	442	16	Human T-cell lymph
3	182	97.8	440	22	Mouse-Human plasma
4	182	97.8	440	22	Mouse-Human plasma
5	182	97.8	441	16	Human acetyl hydro
6	182	97.8	441	16	Human acetyl hydro
7	182	97.8	441	16	Human acetyl hydro
8	182	97.8	441	16	Human acetyl hydro
9	182	97.8	441	16	Human acetyl hydro
10	182	97.8	441	16	Human acetyl hydro
11	182	97.8	441	16	Human acetyl hydro

12	182	97.8	441	16	Human acetyl hydro
13	182	97.8	441	16	Human acetyl hydro
14	182	97.8	441	16	Human acetyl hydro
15	182	97.8	441	16	Human plasma plate
16	182	97.8	441	18	Human platelet-act
17	182	97.8	441	18	Human plasma plate
18	182	97.8	441	18	Human platelet-act
19	182	97.8	441	18	Human plasma plate
20	182	97.8	441	19	Human plasma plate
21	182	97.8	441	20	Human PAF-AH prote
22	182	97.8	441	21	Human platelet-act
23	182	97.8	441	21	Human platelet-act
24	182	97.8	441	21	Human PAF-AH prote
25	182	97.8	441	22	Human plasma plate
26	182	97.8	441	22	Human plasma plate
27	182	97.8	441	22	Human plasma plate
28	182	97.8	441	22	Human plasma plate
29	182	97.8	441	22	Human plasma plate
30	182	97.8	441	22	Human plasma plate
31	182	97.8	441	22	Human plasma plate
32	182	97.8	441	22	Human plasma plate
33	182	97.8	441	22	Human plasma plate
34	182	97.8	441	22	Human plasma plate
35	182	97.8	441	22	Human plasma plate
36	182	97.8	441	22	Human plasma plate
37	182	97.8	441	22	Human plasma plate
38	182	97.8	441	22	Human plasma plate
39	182	97.8	441	22	Human plasma plate
40	163	87.6	171	16	Human plasma plate
41	163	87.6	171	16	Human plasma plate
42	163	87.6	171	18	Human plasma plate
43	163	87.6	171	19	Human plasma plate
44	163	87.6	171	20	Human plasma plate
45	163	87.6	171	20	Human plasma plate

ALIGNMENTS

RESULT 1

AA01942

ID AAB01942 standard; Protein; 441 AA.

XX AAB01942;

AC AAB01942;

XX 18-SEP-2000 (first entry)

XX Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).

DE Human; low density lipoprotein associated phospholipase A2;

XX LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;

XX short chain phospholipid; serine-dependant phospholipase;

XX inflammation; proinflammatory; anti inflammatory; drug screening;

XX antibody; diagnosis.

XX Homo sapiens.

XX WO200024910-A1.

XX 04-MAY-2000.

XX 27-OCT-1999; 99WO-GB03551.

XX 28-OCT-1998; 98GB-0023647.

XX 28-OCT-1998; 98GB-0023648.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Boyd H, Tew DG;

XX WPI; 2000-350749/30.

XX N-PSDB; AAA52357.

XX

PT Recombinant low density lipoprotein associated phospholipase A2, used  
 PT to produce antibodies for diagnostics, is purified using a Blue  
 XX Sepharose and Q Sepharose column -  
 XX  
 PS Claim 6b; Page 17; 28pp; English.

XX The present sequence represents human LDL-PLA2. The invention  
 CC relates to a method for purifying recombinant low density lipoprotein-  
 CC associated phospholipase A2 (LDL-PLA2). The method comprises  
 CC applying a cell extract, supernatant or solution containing the  
 CC recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the  
 CC eluate to a Blue Sepharose column, and applying that eluate to a Q  
 CC Sepharose column. The invention also provides a process which  
 CC additionally comprises the prior steps of constructing a vector  
 CC comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment  
 CC thereof, expressing the tagged protein in a host cell, isolating the  
 CC tagged protein from the harvest medium or cell lysate, purifying the  
 CC protein using a metal matrix affinity column (preferably a nickel  
 CC column), and removing the histidine tag by protease cleavage. LDL-PLA2,  
 CC also known as plasma PAF acetyl hydroxylase, is a serine-dependent  
 CC phospholipase which catalyses the hydrolysis of phospholipids with short  
 CC chain acyl groups at the sn-2 position. Its in vivo role is not known -  
 CC due to its ability to hydrolyse both phospholipids with short chain sn-2  
 CC substituents (which often arise from oxidative cleavage of longer chain  
 CC sn-2 substituents) and PAF, it may be either a pro-inflammatory enzyme or  
 CC an anti-inflammatory enzyme, depending on the precise in vivo role  
 CC adopted. LDL-PLA2 can be used in structural and mechanistic studies to  
 CC elucidate the activity of the enzyme in vivo. The enzyme may be used to  
 CC screen and identify compounds which modulate its activity, and to raise  
 CC antibodies for use in diagnostics.

XX Sequence 441 AA;

Query Match 100.0%; Score 186; DB 21; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQ 37  
 Db 368 mlkkgdidsnaaidlsnkaslatlqkhlghkdfdq 404

RESULT 2

AAR64928  
 ID AAR64928 standard; Protein; 442 AA.

XX AAR64928;

DT 18-AUG-1995 (first entry)

XX Human T-cell lymphoma lipoprotein-associated phospholipase-A2.

DE T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;  
 KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Peptide 25..31 /note= "Peptide 4"  
 FT Peptide 115..133 /note= "Peptide 3"  
 FT Peptide 298..327 /note= "Peptide 2"  
 FT Peptide 368..393 /note= "Peptide 1"

XX W09500649-A.

XX 05-JAN-1995.

XX 24-JUN-1994; 94WO-GB01374.

XX 25-JUN-1993; 93GB-0013144.  
 PR 11-JAN-1994; 94GB-0000413.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Gloger IS, Hickey DMB, Lawrence GMP, Macphree CH;  
 PI Rice SQJ, Southern CD, Tew DG;  
 XX WPI; 1995-052086/07.  
 DR N-PSDB; AAQ81780.

PT Purified lipoprotein associated phospholipase A2 - used to  
 PT develop prods. for diagnosis and therapy, partic. Inhibitors for  
 PT treatment of atherosclerosis  
 XX Claim 8; Page 19; 29pp; English.

XX This sequence encodes an enzyme which may be used in a method of  
 CC screening compounds to identify those compounds which inhibit  
 CC Lp-PLA2 which involves contacting isolated Lp-PLA2 with a test  
 CC compound and measuring the rate of turnover of an enzyme substrate  
 CC as compared with the rate of turnover in the absence of the test  
 CC compound.

XX Sequence 442 AA;

Query Match 100.0%; Score 186; DB 16; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQ 37  
 Db 368 mlkkgdidsnaaidlsnkaslatlqkhlghkdfdq 404

RESULT 3

AAE00782  
 ID AAE00782 standard; Protein; 440 AA.

XX AAE00782;

DT 02-JUL-2001 (first entry)

XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC1.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parcutition;  
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..97 /note= "Corresponds to N-terminal 97 amino acids of mouse  
 FT plasma platelet-activating factor acetylhydrolase  
 FT (PAF-AH)"  
 FT Region 98..440 /note= "Corresponds to C-terminal 343 amino acids of  
 FT human plasma platelet-activating factor acetylhydrolase  
 FT (PAF-AH)"

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

XX 22-JAN-1998; 98US-0010715.

XX 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

PI Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

XX Wilder CL;

XX WPI; 2001-280610/29.

XX N-PSDB; AAD04168.

XX Treating a mammal susceptible to or suffering from septicemia comprises  
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
PT supplement endogenous PAF-AH activity and to inactivate pathological  
PT amounts of PAF -

XX Example 8; Column -: 54pp; English.

XX The present sequence is mouse-human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid  
XX PRC/PH.MHC1.

XX The invention relates to human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
XX invention also relates to method of treating a mammal susceptible to  
XX or suffering from septicemia. PAF functions in normal physiological  
XX processes such as inflammation, haemostasis and parturition. PAF-AH  
XX specific antibodies are used in the diagnostic methods to detect abnormal  
XX levels of PAF-AH in serum and also for treating the pathological  
XX inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
XX shock and arthritis. PAF-AH antibody is also useful for screening a  
XX genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
XX replacement of nucleotide G to T at position 996 within exon 9 resulting  
XX in replacement of amino acid Val to Phe at position 279. Thus the  
XX deficiency of PAF-AH activity is due to the genetic lesion in human  
XX plasma PAF-AH gene.

XX Sequence 440 AA;

Query Match 97.8%; Score 182; DB 22; Length 440;

Best Local Similarity 97.3%; Pred. No. 1.5e-18;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASIAFLQKHLGLHKDFDQ 37

Db 367 mlklkgidsnvaidslnkasiaflqlkhlghkdfdq 403

RESULT 4

AAE00783

ID AAE00783 standard; Protein; 440 AA.

XX AC AAE00783;

XX 02-JUL-2001 (first entry)

XX Mouse-Human plasma PAF-AH fusion protein from plasmid PRC/PH.MHC2.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
XX antiinflammatory; septicemia; inflammation; haemostasis; parturition;  
XX asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..40

XX /note= "Corresponds to N-terminal 40 amino acids of mouse  
XX plasma platelet-activating factor acetylhydrolase  
XX (PAF-AH)"

XX Region 41..440

XX /note= "Corresponds to C-terminal 400 amino acids of  
XX human plasma platelet-activating factor acetylhydrolase  
XX (PAF-AH)"

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

XX 22-JAN-1998; 98US-0010715.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

XX WPI; 2001-280610/29.

XX N-PSDB; AAD04169.

XX Treating a mammal susceptible to or suffering from septicemia comprises  
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
PT supplement endogenous PAF-AH activity and to inactivate pathological  
PT amounts of PAF -

XX Example 8; Column -: 54pp; English.

XX The present sequence is mouse-human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid  
XX PRC/PH.MHC2.

XX The invention relates to human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
XX invention also relates to method of treating a mammal susceptible to  
XX or suffering from septicemia. PAF functions in normal physiological  
XX processes such as inflammation, haemostasis and parturition. PAF-AH  
XX specific antibodies are used in the diagnostic methods to detect abnormal  
XX levels of PAF-AH in serum and also for treating the pathological  
XX inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
XX shock and arthritis. PAF-AH antibody is also useful for screening a  
XX genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
XX replacement of nucleotide G to T at position 996 within exon 9 resulting  
XX in replacement of amino acid Val to Phe at position 279. Thus the  
XX deficiency of PAF-AH activity is due to the genetic lesion in human  
XX plasma PAF-AH gene.

XX Sequence 440 AA;

Query Match 97.8%; Score 182; DB 22; Length 440;

Best Local Similarity 97.3%; Pred. No. 1.5e-18;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASIAFLQKHLGLHKDFDQ 37

Db 367 mlklkgidsnvaidslnkasiaflqlkhlghkdfdq 403

RESULT 5

AAE73048

ID AAE73048 standard; Protein; 441 AA.

XX AC AAE73048;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C291S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 291 /note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKHDFDQ 37  
Db ||||||||| ||||||||| ||||||||| ||||||||| |||||||||  
368 mlkkgidsnvaidsnksaslaflqkhlgkhdfdq 404

RESULT 6

AAR73049  
ID AAR73049 standard; Protein; 441 AA.

XX AAR73049;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C334S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Misc-difference 334

FT /note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKHDFDQ 37  
Db ||||||||| ||||||||| ||||||||| ||||||||| |||||||||  
368 mlkkgidsnvaidsnksaslaflqkhlgkhdfdq 404

RESULT 7

AAR73050  
ID AAR73050 standard; Protein; 441 AA.

XX AAR73050;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C407S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Misc-difference 407

FT /note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating



PT inflammatory diseases, e.g. pleurisy  
 XX Example 10; : 88pp; English.  
 PS  
 CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKLGKIDISNAIDLSNKSALFLQKHLGLHKDFDQ 37  
 |||||  
 Db 368 mlklkgidsnvaidsnksalflqkhlghlkdfdq 404

RESULT 8  
 AAR71920  
 ID AAR71920 standard; Protein; 441 AA.  
 XX  
 AC AAR71920;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant S108A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."  
 FT  
 XX WO9509921-A.  
 XX  
 PD 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; : 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKLGKIDISNAIDLSNKSALFLQKHLGLHKDFDQ 37  
 |||||  
 Db 368 mlklkgidsnvaidsnksalflqkhlghlkdfdq 404

RESULT 9  
 AAR71921  
 ID AAR71921 standard; Protein; 441 AA.  
 XX  
 AC AAR71921;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant S273A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."  
 FT  
 XX WO9509921-A.  
 XX  
 PD 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; : 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;

AAR/1923;  
06-DEC-1995 (first entry)

[illegible]

acetyl hydrolase; AN; platelet activating factor; PAF; inflammatory disease; pleurisy; diagnosis.

**Homo sapiens.**

Key  
Location/Qualifiers  
Misc-difference 338

/note= "Wild-type Asp is substd. by Ala."

W09509921-A.  
13-APR-1995

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00-001-1993; 9303-0133803.

(ICOS-) ICOS CORP.

Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

— 200 —

MMPT; 1993-1997

New nucleic acid encoding platelet activating factor, acetyl-hydrolase - useful in diagnosis and for treating

inflammatory diseases, e.g. pleurisy

Example 10; ; 88pp; English.

The human acetyl hydrolase (AH) gene (AA087947) has been isolated and

purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were made with single amino acid changes for the purposes of identifying

the active site of AH. The sequences of these mutants are not given

wild-type protein (AAR71913).

The an gene and its products are useful in the treatment of inflammatory diseases, in particular pleurisy, asthma, rhinitis and eczema. The

gene may also be used in raising monoclonal antibodies specific for AH that are useful in the diagnosis of such diseases

[illegible]

very Match 97.88; Score 182; DB 16; Length 441;

st Local Similarity 97.38; pred. No. 1.5e-18;  
ches 36: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

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[illegible]

JUL 12 1924

1524 AAR71924 standard; Protein: 441 AA.

AAR71924;

06-DEC-1995 (first entry)

Human acetyl hydrolysis mutant H351A

Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory disease; pleurisy; diagnosis

strong, arduous.

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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 351
PT /note= "Wild-type His is substd. by Ala."
XX
XX WO9509921-A.
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XX 13-APR-1995.
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XX 06-OCT-1994; 94WO-US11340.
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XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX
XX Example 10; ; 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
XX in the patent specification; they have been derived from the original
XX wild-type protein (AAR71913).
XX
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKIKGDISNAADLSNKSALFLQKHLGHLKDFDQ 37
Db 368 mlklkgdisnvaidslnksalflqkhlglbkdfdq 404

RESULT 13
AAR73046
ID AAR73046 standard; Protein; 441 AA.
XX
XX AAR73046;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C67S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 67
XX /note= "Wild-type Cys is substd. by Ser."
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
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PF 06-OCT-1994; 94WO-US11340.
PR 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX
XX Example 10; ; 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
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XX wild-type protein (AAR71913).
XX
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKIKGDISNAADLSNKSALFLQKHLGHLKDFDQ 37
Db 368 mlklkgdisnvaidslnksalflqkhlglbkdfdq 404

RESULT 14
AAR73047
ID AAR73047 standard; Protein; 441 AA.
XX
XX AAR73047;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C229S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 229
XX /note= "Wild-type Cys is substd. by Ser."
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX

```

XX PT New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy  
XX PS  
XX Example 10; : 88pp; English.  
XX CC  
CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).  
CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.  
XX CC  
XX SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQ 37  
|||||  
Db 368 mlkkgdidsnvaidsnksaslaflqkhlghkdfdq 404

## RESULT 15

AAR71913  
ID AAR71913 standard; Protein; 441 AA.

XX AC AAR71913;

DT 05-DEC-1995 (first entry)

DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

XX ACetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX PN WO9509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder Ct;

XX DR WPI; 1995-155252/20.

XX DR N-PSDB; AA087947.

XX PT New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy  
XX PT

PS Claim 5; Page 53-54; 88pp; English.

XX CC The human acetyl hydrolase gene (AA087947) has been isolated and  
CC purified. The platelet activating factor acetyl hydrolase (AAR71913)  
CC is useful in the treatment of inflammatory diseases, in particular  
CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in  
CC raising monoclonal antibodies specific for PAF-AH that are useful in  
CC the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;  
Best Local Similarity 97.3%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQ 37  
|||||  
Db 368 mlkkgdidsnvaidsnksaslaflqkhlghkdfdq 404

Search completed: March 9, 2002, 00:31:56  
Job time: 442 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:26:19 : Search time 47.03 Seconds  
(without alignments)  
17.704 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186

Sequence: 1 MLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQ 37

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA.\*
- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	37	2	US-08-557-892-1
2	186	100.0	37	2	US-08-387-858A-1
3	186	100.0	37	4	US-09-294-384B-1
4	182	97.8	441	1	US-08-470-187-8
5	182	97.8	441	1	US-08-318-905-8
6	182	97.8	441	1	US-08-483-232-8
7	182	97.8	441	1	US-08-483-140-8
8	182	97.8	441	2	US-08-485-938A-8
9	182	97.8	441	2	US-08-910-041-8
10	182	97.8	441	3	US-09-328-474-8
11	182	97.8	441	3	US-09-100-546-8
12	182	97.8	441	4	US-09-010-715-8
13	182	97.8	441	4	US-09-577-758-8
14	163	87.6	171	1	US-08-483-140-29
15	163	87.6	171	2	US-08-485-938A-35
16	155	83.3	444	1	US-08-483-140-28
17	155	83.3	444	2	US-08-485-938A-32
18	155	83.3	444	2	US-08-485-938A-33
19	148	79.6	440	1	US-08-483-140-27
20	148	79.6	440	2	US-08-485-938A-31
21	128	68.8	422	2	US-08-485-938A-34
22	73	39.2	392	2	US-08-886-152-1
23	71	38.2	392	2	US-08-886-152-3
24	52	28.0	419	1	US-08-330-154-2
25	51	27.4	2252	4	US-09-091-219-25
26	51	27.4	2247	4	US-09-091-219-2
27	51	27.4	15281	2	US-08-471-119A-2

Sequence 2, Appli  
Sequence 24, Appli  
Sequence 4, Appli  
Sequence 26, Appli  
Sequence 41, Appli  
Sequence 38, Appli  
Sequence 7, Appli  
Sequence 17, Appli  
Sequence 23, Appli  
Sequence 186, App  
Patent No. 5290690  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 2, Appli

28 50.5 27.2 2285 4 US-09-308-375-2  
29 49 26.3 972 3 US-08-335-844A-24  
30 48.5 26.1 2154 2 US-08-841-349-4  
31 47 25.3 509 3 US-08-369-832C-26  
32 47 25.3 509 3 US-08-582-776C-41  
33 47 25.3 509 3 US-08-434-831B-38  
34 46 24.7 92 1 US-08-347-492B-7  
35 46 24.7 92 2 US-08-798-143-7  
36 46 24.7 862 3 US-09-315-861-2  
37 46 24.7 1098 4 US-08-946-994-17  
38 46 24.7 1561 3 US-08-894-017-23  
39 45.5 24.5 1494 3 US-08-755-587-186  
40 45 24.2 334 6 5290690-11  
41 45 24.2 881 4 US-09-413-814-44  
42 44.5 23.9 389 3 US-08-972-902-4  
43 44.5 23.9 428 2 US-08-889-711-4  
44 44.5 23.9 428 3 US-09-185-823-4  
45 44.5 23.9 763 2 US-08-889-711-2

ALIGNMENTS

RESULT 1

US-08-557-892-1  
; Sequence 1, Application US/08557892  
; Patent No. 5968818  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/08/557.892  
; FILING DATE: 14 No. 5968818ember 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387.858  
; FILING DATE: 14 No. 5968818ember 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: F30693C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE:

FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
FEATURE:  
US-08-557-892-1

Query Match 100.0%; Score 186; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.6e-21;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37  
Db 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37

RESULT 2  
US-08-387-858A-1  
; Sequence 1, Application US/08387858A  
; Patent No. 5981252  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Glover, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/08/387,858A  
; APPLICATION NUMBER: US/08/387,858A  
; FILING DATE: 24 February 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/01374  
; FILING DATE: 24 June 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; FEATURE:

US-08-387-858A-1

Query Match 100.0%; Score 186; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.6e-21;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37  
Db 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37

RESULT 3  
US-09-294-384B-1  
; Sequence 1, Application US/09294384B  
; Patent No. 6177257  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Glover, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/09/294,384B  
; APPLICATION NUMBER: US/09/294,384B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,858  
; FILING DATE: 24 February 1995  
; APPLICATION NUMBER: PCT/GB94/01374  
; FILING DATE: 24 June 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; FEATURE:

US-09-294-384B-1

Query Match 100.0%; Score 186; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.6e-21;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37  
Db 1 MLKLGIDSNAAIDLSNKKASLAFLOKHLGHRDQ 37



RESULT 4  
US-08-470-187-8  
; Sequence 8, Application US/08470187  
; Patent No. 5532152  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,187  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5532152and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-470-187-8

Query Match 97.8%; Score 182; DB 1; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.1e-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKLGDISNAADLSNKLAFLOKHLGKDFDQ 37  
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Db 368 MLKLGDISNVAIDLSNKLAFLOKHLGKDFDQ 404

RESULT 5  
US-08-318-905-8  
; Sequence 8, Application US/08318905  
; Patent No. 5641669  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,905  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5641669and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-318-905-8

Query Match 97.8%; Score 182; DB 1; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.1e-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGDISNAADLSNKLAFLOKHLGKDFDQ 37  
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Db 368 MLKLGDISNVAIDLSNKLAFLOKHLGKDFDQ 404

RESULT 6  
US-08-483-232-8  
; Sequence 8, Application US/08483232  
; Patent No. 5656431  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,232

; FILING DATE: 435  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 565643land, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-232-8

Query Match 97.8%; Score 182; DB 1; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.1e-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 1 MLKLGKGDSDNAADLSNKAFLQKHGLHKDFDQ 37  
Db 368 MLKLGKGDSDNVAIDLSNKAFLQKHGLHKDFDQ 404

RESULT 7  
US-08-483-140-8  
; Sequence 8, Application US/08483140  
; Patent No. 5698403  
; GENERAL INFORMATION:  
; APPLICANT: ICOS Corporation  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,140  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 6-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5698403and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32781  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658

; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-140-8

Query Match 97.8%; Score 182; DB 1; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.1e-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 1 MLKLGKGDSDNAADLSNKAFLQKHGLHKDFDQ 37  
Db 368 MLKLGKGDSDNVAIDLSNKAFLQKHGLHKDFDQ 404

RESULT 8  
US-08-485-938A-8  
; Sequence 8, Application US/08485938A  
; Patent No. 5847088  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S. D.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,938A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5847088and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32792  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-485-938A-8

Query Match 97.8%; Score 182; DB 2; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.1e-19;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MLKLKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 37  
Db 368 MLKLKGDIDSNVAIDLSNKASLAFLQKHLGKDFDQ 404

## RESULT 9

US-08-910-041-8  
; Sequence 8, Application US/08910041  
; Patent No. 5977308  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,041  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/483,232  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rin-Laures, Li-Hsien  
; REGISTRATION NUMBER: 33,547  
; REFERENCE/DOCKET NUMBER: 27866/34026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-910-041-8

Query Match 97.8%; Score 182; DB 2; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.le-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MLKLKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 37  
Db 368 MLKLKGDIDSNVAIDLSNKASLAFLQKHLGKDFDQ 404

## RESULT 10

US-09-328-474-8  
; Sequence 8, Application US/09328474  
; Patent No. 6045794  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/328,474  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/483,232  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rin-Laures, Li-Hsien  
; REGISTRATION NUMBER: 33,547  
; REFERENCE/DOCKET NUMBER: 27866/34026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-328-474-8

Query Match 97.8%; Score 182; DB 3; Length 441;  
Best Local Similarity 97.3%; Pred. No. 2.le-19;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MLKLKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 37  
Db 368 MLKLKGDIDSNVAIDLSNKASLAFLQKHLGKDFDQ 404

## RESULT 11

US-09-100-546-8  
; Sequence 8, Application US/09100546  
; Patent No. 6099836  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai

APPLICANT: Toeelker, Larry W.  
 APPLICANT: Wilder, Cheryl L.  
 TITLE OF INVENTION: platelet-Activating Factor  
 TITLE OF INVENTION: Acetylhydrolase  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER TYPE: FLOPPY disk  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/100,546  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/010,715  
 FILING DATE:  
 APPLICATION NUMBER: US 08/318,905  
 FILING DATE: 06-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/133,803  
 FILING DATE: 06-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6099836and, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/32793  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3658  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 441 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PS-09-100-546-8

	Query Match	97.88;	Score 182;	DB 3;	Length 441;
	Best Local Similarity	97.3%;	Pred. No. 2.le-19;		
	Matches 36;	Conservative	0;	Mismatches 1;	Indels
QY	1	MLKLGKDIDSNAAIDLNSKASLAFLOKHGLGHRDFDQ	37		
DB	368	MLKLGKDIDSNVAIDLNSKASLAFLOKHGLGHRDEDO	404		

RESULT 12  
US-09-010-715-8  
: Sequence 8, Application US/09010715  
: Patent No. 6146623  
: GENERAL INFORMATION:  
: APPLICANT: Cousins, Lawrence S.  
: APPLICANT: Eberhardt, Christine D.  
: APPLICANT: Gray, Patrick W.  
: APPLICANT: Le Trong, Hai  
: APPLICANT: Tjoelker, Larry W.  
: APPLICANT: Wilder, Cheryl L.  
: TITLE OF INVENTION: Platelet-Activating Factor  
: NUMBER OF SEQUENCES: 30  
: NUMBER OF INVENTIONS: 30  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: STREET: 6300 Sears Tower, 233 South Wacker Drive  
: CITY: Chicago

```

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 614862sand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 97.8%; Score 182; DB 4;
Best Local Similarity 97.3%; Pred. NO. 2.le-19;
Matches 36; Conservative 0; Mismatches 1;

QY 1 MLKLGKGDIDSNAAIDLSNKNASIAFLAQKHLGLHKDFDQ 37
|||||
DB 368 MLKLGKGDIDSNVAIDLSNKNASIAFLAQKHLGLHKDFDQ 404
|||||

RESULT 13
US-09-577-758-8
Sequence 8, Application US/095777758
Patent No. 6203790
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry L.
APPLICANT: Wilder, Cheryl W.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray
CITY: 6300 Sears Tower, 233 South Wacker Drive
STREET: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,758
FILING DATE:

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Search completed: March 9, 2002, 00:32:58  
Job time: 399 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:28:49 ; Search time 53.53 Seconds  
(without alignments)  
52.652 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186

Sequence: 1 MLKLGKIDSNAAIDLSNKNASLAFLQKHLG:HKDFDQ 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	97.8	441	2 S60247	platelet-activatin
2	135	72.6	436	2 JC5021	platelet-activatin
3	53	28.5	333	2 C85737	glycerolaldehyde-3-p
4	53	28.5	736	2 T01247	hypothetical prote
5	52.5	28.2	755	2 T34567	hypothetical prote
6	52	28.0	165	2 S14477	glycerolaldehyde-3-p
7	52	28.0	422	2 JC5325	methicillin resist
8	51	27.4	306	1 S39151	cyclin-suppressing
9	51	27.4	433	2 S06783	fema protein: Sta
10	51	27.4	488	2 F84001	glycine dehydrogen
11	51	27.4	650	2 T04416	sulfate transport
12	51	27.4	698	2 A54796	regulatory protein
13	51	27.4	15281	2 S41309	cyclosporin synthet
14	50.5	27.2	266	2 E64471	hypothetical prote
15	50.5	27.2	395	2 A37118	hypothetical prote
16	50.5	27.2	758	2 S47866	methionine adenosy
17	50.5	27.2	2285	2 T12796	SPT21 protein - ve
18	50	26.9	115	2 A68853	probable transglyc
19	50	26.9	549	2 A39345	hypothetical prote
20	50	26.9	587	1 W2BEC9	alpha-mannosidase
21	49.5	26.6	441	2 A45565	gene 36 protein -
22	49	26.3	145	2 S62510	cysteine proteinas
23	49	26.3	175	2 B69250	hypothetical prote
24	49	26.3	260	2 E69956	hypothetical prote
25	49	26.3	285	2 T05777	phosphate ABC tran
26	49	26.3	333	1 DEHGGT	hypothetical prote
27	49	26.3	374	2 T44696	glycerolaldehyde-3-p
28	49	26.3	377	1 A44216	hypothetical prote
29	49	26.3	513	2 S65574	major envelope ant
					phosphate transpor

30 49 26.3 558 2 B82976 membrane protein c  
31 49 26.3 587 2 T42580 gene 36 protein -  
32 49 26.3 652 2 T19783 hypothetical prote  
33 49 26.3 1151 1 S45390 protein kinase C (  
34 48.5 26.1 182 2 F81366 adenine phosphorib  
35 48.5 26.1 395 1 S27257 methionine adenosy  
36 48.5 26.1 464 2 C86422 probable glycy-l-tr  
37 48.5 26.1 2364 1 A44159 spectrin beta-G ch  
38 48 25.8 244 2 T22779 hypothetical prote  
39 48 25.8 321 2 B71950 hypothetical prote  
40 48 25.8 338 2 T09633 glycerolaldehyde-3-p  
41 48 25.8 556 2 S49754 probable membrane  
42 48 25.8 1609 2 A86611 probable outer mem  
43 48 25.8 1609 2 H72013 polymorphic membra  
44 47.5 25.5 277 2 S34146 porin porl, plasti  
45 47.5 25.5 335 2 T31177 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf,

W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:G780132; PIDN:AAC50126.1; PID:G780133

##### Query Match

Best Local Similarity 97.8%; Score 182; DB 2; Length 441;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKIDSNAAIDLSNKNASLAFLQKHLG:HKDFDQ 37

DB 368 MLKLGKIDSNAAIDLSNKNASLAFLQKHLG:HKDFDQ 404

##### RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAR-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C:Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoy

J.; Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KAR1>

A:Cross-references: DDBJ:D67037; NID:G1644228; PIDN:BAAL1054.1; PID:G1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>

F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.6%; Score 135; DB 2; Length 436;  
Best Local Similarity 75.7%; Pred. No. 7.3e-11;  
Matches 28; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASLAFLOKHLGHLKDFDQ 37

Db 366 MSLKGIKIDSEVANDLINKASLAFLOKHLGHLKDFDQ 402

## RESULT 3

C85737  
glyceraldehyde-3-phosphate dehydrogenase [imported] - Escherichia coli (strain O157:H7)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
C:Accession: C85737  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: C85737  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-333 <STO>  
A:Cross-references: GB:AE005174; NID:g12515293; PIDN:AA056359.1; GSPDB:GN00145; UWGP:Z2  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: gapC  
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 28.5%; Score 53; DB 2; Length 333;  
Best Local Similarity 42.9%; Pred. No. 12;  
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASLAFLOKHL 28

Db 20 LLEVKSNIDVVAINDLTPKILAYLLKH 47

## RESULT 4

T01247  
hypothetical protein At2g38150 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F16M14.8  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 23-Mar-2001  
C:Accession: T01247; E04801  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, July 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.  
A:Reference number: Z14213  
A:Accession: T01247  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-736 <ROU>  
A:Cross-references: EMBL:AC003028; NID:g3335363; PID:g3335363  
A:Experimental source: cultivar Columbia  
R:Lip, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: E04801  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-736 <STO>  
A:Cross-references: GB:AE002093; NID:g3335363; PIDN:AC27164.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g38150; F16M14.8  
A:Map position: 2  
A:Introns: 63/3; 107/1; 356/1

C:Superfamily: Arabidopsis thaliana hypothetical protein At2g38150

Query Match 28.5%; Score 53; DB 2; Length 736;  
Best Local Similarity 54.5%; Pred. No. 28;  
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 15 DLSNKASLAFLOKHLGHLKDFD 36

Db 193 NLSNLARLAFUYKGGVILDTD 214

## RESULT 5

T34567  
hypothetical protein DKFZp434A128.1 - human  
C:Species: Homo sapiens (man)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T34567  
R:Ottewälder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, October 1999  
A:Reference number: Z21542  
A:Accession: T34567  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-755 <OTT>  
A:Cross-references: EMBL:AL122120  
A:Experimental source: adult testis; clone DKFZp434A128  
C:Genetics:  
A:Note: DKFZp434A128.1

Query Match 28.2%; Score 52.5; DB 2; Length 755;  
Best Local Similarity 28.6%; Pred. No. 34;  
Matches 14; Conservative 10; Mismatches 12; Indels 13; Gaps 2;

QY 1 MLKLKGDIDSNAAIDLSN-----KASLAFLOKHLGHLKDFDQ 37

Db 318 MOKRGDGDID-NCALELARIKQETREKNLVREKTFLEISEIGNNTEFEK 365

## RESULT 6

S14477  
glyceraldehyde-3-phosphate dehydrogenase homolog - rat (fragment)  
N:Alternate names: glyceraldehyde-3-phosphate dehydrogenase-like protein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Jun-1999  
C:Accession: S14477; A24915  
R:Krawetz, S.A.; Connor, W.; Dixon, G.H.  
submitted to the EMBL Data Library, October 1990  
A:Reference number: S14477  
A:Accession: S14477  
A:Molecule type: mRNA  
A:Residues: 1-165 <KRA1>  
A:Cross-references: EMBL:X54798; NID:g57571; PIDN:CAA38569.1; PID:g57572  
R:Krawetz, S.A.; Connor, W.; Cannon, F.D.; Dixon, G.H.  
DNA 5, 427-435, 1986  
A:Title: A vector-primer-cloner-sequencer plasmid for the construction of cDNA 11  
A:Reference number: A24915; MUID:87053179  
A:Accession: A24915  
A:Molecule type: mRNA  
A:Residues: 1-52 <KRA>  
A:Cross-references: GB:M14166; NID:g204191; PIDN:AAA1178.1; PID:g204192  
C:Genetics:  
A:Gene: G3PD  
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 28.0%; Score 52; DB 2; Length 165;  
Best Local Similarity 42.9%; Pred. No. 7.2;  
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASLAFLOKH 28

Db 1 MLKLKGDIDSNAAIDLSNKASLAFLOKH 28



Db 20 LLEVKSNIDVVAINDLTSPIILAYLLKH 47

## RESULT 7

JC5325  
methicillin resistance factor FEMA - Staphylococcus epidermidis  
C:Species: Staphylococcus epidermidis  
C:Date: 15-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 07-May-1999  
C:Accession: JC5325; PC4317  
R:Alborn Jr., W.E.; Hoskins, J.; Uenal, S.; Flokowitsch, J.E.; Hayes, C.A.; Dotzlauf, J.E.  
Mol. Gen. Genet. 219, 263-269, 1989  
A:Title: Cloning and characterization of femA and femB from Staphylococcus epidermidis.  
A:Reference number: JC5325; MUID:97128824  
A:Accession: JC5325  
A:Molecule type: DNA  
A:Residues: 1-422 <ALE>  
A:CROSS-references: GB:U23713  
A:Accession: PC4317  
A:Molecule type: protein  
A:Residues: 1-20 <AL2>  
C:Genetics:  
A:Gene: femA  
C:Superfamily: methicillin resistance factor femA

Query Match 28.0%; Score 52; DB 2; Length 422;

Best Local Similarity 40.5%; Pred. No. 21; Mismatches 15; Indels 4; Gaps 2;

QY 2 LRLKGDIDNSNAID--LSNKASLAFLOKHLGLHKDFD 36

Db 121 LNHEGEGTGNAGHDWIFDELSGY--KHGEGFKGFD 155

## RESULT 8

S39151  
cyclin-suppressing protein kinase csk1 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces  
C:Species: Schizosaccharomyces pombe  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Dec-1999  
C:Accession: S39151; T38047  
R:Molz, L.; Beach, D.  
EMBO J. 12, 1723-1732, 1993  
A:Title: Characterization of the fission yeast mcs2 cyclin and its associated protein k  
A:Reference number: S35380; MUID:93223713  
A:Accession: S39151  
A:Molecule type: DNA  
A:Residues: 1-306 <MOL>  
A:CROSS-references: GB:S59896; NID:g299548; PIDN:AA826194.1; PID:g299549  
R:Lye, G.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, February 1995  
A:Reference number: Z21765  
A:Accession: T38047  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 <LYE>

A:CROSS-references: EMBL:269239; PIDN:CAA93215.1; GSPDB:GN00066; SPDB:SPAC1D4.06c

A:Experimental source: strain 972h; cosmid c1d4

C:Genetics:

A:Gene: csk1; SPAC1D4.06c

A:Map position: 1

A:introns: 168/3; 240/3

C:Superfamily: fission yeast cyclin kinase csk1; protein kinase homology

C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

F:9-268/Domain: protein kinase homology <KIN>

Query Match 27.4%; Score 51; DB 1; Length 306;

Best Local Similarity 40.7%; Pred. No. 20;

Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 IDSNAIDLSNKASLAFLOKHLGLHKD 34

Db 103 IDTKCKIVLQISSALEYKHLGILHRD 129

## RESULT 9

S06783  
femA protein - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Sep-1999  
C:Accession: S06783  
R:Berger-Baechi, B.; Barberis-Maino, L.; Straessle, A.; Kayser, F.H.  
Mol. Gen. Genet. 219, 263-269, 1989  
A:Title: FemA, a host-mediated factor essential for methicillin resistance in Staphy  
A:Reference number: S06782; MUID:90136516  
A:Accession: S06783  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-433 <BER>  
A:CROSS-references: EMBL:X17688; NID:g46579; PIDN:CAA35679.1; PID:g46581  
C:Genetics:  
A:Gene: femA  
A:Map position: 18 min  
C:Superfamily: methicillin resistance factor femA  
C:Keywords: antibiotic resistance

Query Match 27.4%; Score 51; DB 2; Length 433;

Best Local Similarity 39.4%; Pred. No. 29;

Matches 13; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

QY 6 GDIDSNAID--LSNKASLAFLOKHLGLHKDFD 36

Db 133 GEITGNAGNDWFFDKMSNLGF--ERTGFHKGFD 163

## RESULT 10

F84001  
glycine dehydrogenase subunit 2 BH2814 [imported] - Bacillus halodurans (strain C-12  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: F84001  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans  
A:Reference number: AB9650; MUID:20263314  
A:Accession: F84001  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-488 <STO>  
A:CROSS-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA806533.1; GSPDB:  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2814

Query Match 27.4%; Score 51; DB 2; Length 488;

Best Local Similarity 37.0%; Pred. No. 34;

Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 9 DSNAIDLSNKASLAFLOKHLGLHKDF 35

Db 249 NSNAILGIARPGDMGFDVVHLNLHKTF 275

## RESULT 11

T04416  
sulfate transport protein ST1, high affinity - barley  
C:Species: Hordeum vulgare (barley)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 01-Dec-2000  
C:Accession: T04416; T05742  
R:Vidmar, J.J.; Schjoerring, J.K.; Glass, A.D.M.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z15351  
A:Accession: T04416  
A:Status: preliminary; translated from GB/EMBL/DBJ



Search completed: March 9, 2002, 00:34:07  
Job time: 318 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:19 ; Search time 30.16 seconds  
(without alignments)  
44,980 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186

Sequence: 1 MLKLKGDIDSNAAIDLSNKSALFLQHLGLHDKDFDQ 37

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	97.8	441	1 PAPA_HUMAN	Q13093 h platelet-
2	155	83.3	444	1 PAPA_BOVIN	Q28017 b platelet-
3	155	83.3	444	1 PAPA_CANFA	Q28262 c platelet-
4	148	79.6	440	1 PAPA_MOUSE	Q60963 m platelet-
5	135	72.6	436	1 PAPA_CAVPO	P70683 c platelet-
6	128	68.8	422	1 PAPA_CHICK	Q90678 g platelet-
7	73	39.2	392	1 PAF2_BOVIN	P79106 bos taurus
8	71	38.2	392	1 PAF2_HUMAN	Q99487 homo sapien
9	53	28.5	333	1 G3P3_ECO57	P58072 escherichia
10	53	28.5	333	1 G3P3_ECOLI	P33898 escherichia
11	51	27.4	306	1 CSK1_SCHPO	P36615 schizosacch
12	51	27.4	433	1 FENA_STAUA	P14304 staphylococ
13	51	27.4	637	1 CRAC_DICDI	P35401 dictyosteli
14	50.5	27.2	395	1 METK_RAT	P18298 rattus norv
15	50.5	27.2	758	1 SP21_YEAST	P35209 saccharomyc
16	50	26.9	549	1 MNS1_YEAST	P32906 saccharomyc
17	50	26.9	587	1 UL25_HSVB	P28928 equine herp
18	49.5	26.6	441	1 CYSF_THEAN	P55781 theileria a
19	49.5	26.6	2156	1 ORPL_HUMAN	P56715 homo sapien
20	49	26.3	145	1 YAF4_SCHPO	Q09588 schizosacch
21	49	26.3	175	1 Y002_ARCFU	Q30233 archaeglob
22	49	26.3	260	1 YQSK_BACSU	P46342 bacillus su
23	49	26.3	332	1 G3P_THEMA	P17721 thermotoga
24	49	26.3	377	1 VENV_FOWPV	P36316 fowlpox vir
25	49	26.3	971	1 AMPN_HAECO	Q10737 haemochus
26	49	26.3	1151	1 KPCL_YEAST	P24583 saccharomyc
27	48.5	26.1	395	1 METK_HUMAN	P31153 homo sapien
28	48.5	26.1	2363	1 SPCO_MOUSE	Q02261 mus musculu
29	48.5	26.1	2364	1 SPCO_MOUSE	Q01082 homo sapien
30	48.5	26.1	4644	1 DYHC_MOUSE	Q9jhu4 mus musculu
31	48	25.8	338	1 G3P_LACDE	Q32755 lactobacill
32	48	25.8	556	1 YMC3_YEAST	Q03718 saccharomyc
33	48	25.8	1609	1 PM21_CHLPM	Q9z6u5 chlamydia p

34 47.5 25.5 277 1 PORI\_MAIZE  
35 47.5 25.5 386 1 ICEA\_XENLA  
36 47.5 25.5 416 1 YTNL\_BACSU  
37 47.5 25.5 1211 1 EX5B\_HAEIN  
38 47 25.3 264 1 GIDB\_SYNY3  
39 47 25.3 390 1 Y109\_NPVAC  
40 47 25.3 400 1 CSD\_METTH  
41 47 25.3 447 1 Y341\_CHLMO  
42 47 25.3 1244 1 SLAI\_YEAST  
43 47 25.3 1966 1 MYSB\_CAEEL  
44 47 25.3 2204 1 RPLD\_NDVB  
45 47 25.3 2216 1 YCF2\_EPVI

## ALIGNMENTS

RESULT 1  
PAPA\_HUMAN  
ID PAPA\_HUMAN STANDARD; PRT: 441 AA.  
AC Q13093; Q15692;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
GN PLA2G7 OR PAFAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
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RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.  
RC TISSUE=Myeloid;  
RX MEDLINE=95214779; PubMed=7700381;  
RA Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,  
RA Schlumpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,  
RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;  
RA "Anti-inflammatory properties of a platelet-activating factor  
acetylhydrolase.";  
[2]  
Nature 374:549-553(1995).  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Lymphoma;  
RX MEDLINE=96197208; PubMed=8624782;  
RA Tew D.G., Southan C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,  
RA Moores K., Gloger I.S., Macphie C.H.;  
RA "Purification, properties, sequencing, and cloning of a lipoprotein-  
associated, serine-dependent phospholipase involved in the oxidative  
modification of low-density lipoproteins.";  
RA Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).  
[3]  
RP MUTAGENESIS.  
RX MEDLINE=96029630; PubMed=7592717;  
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
RA Gray P.W.;  
RA "Plasma platelet-activating factor acetylhydrolase is a secreted  
phospholipase A2 with a catalytic triad.";  
RL J. Biol. Chem. 270:25481-25487(1995).  
[4]  
RP VARIANT PHE-279.  
RX MEDLINE=96259525; PubMed=8675689;  
RA Stafforini D.M., Satch K., Atkinson D.L., Tjoelker L.W.,  
RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,  
RA McIntyre T.M., Gray P.W., Prescott S.M.;  
RA "Platelet-activating factor acetylhydrolase deficiency. A missense  
mutation near the active site of an anti-inflammatory  
phospholipase.";  
RL J. Clin. Invest. 97:2784-2791(1996).  
[5]



PAPA\_CANFA STANDARD; PRT; 444 AA.  
ID PAPA\_CANFA  
AC Q28262;  
AD 01-NOV-1997 (Rel. 35, Created)  
AE 01-NOV-1997 (Rel. 35, Last sequence update)  
AF 20-AUG-2001 (Rel. 40, Last annotation update)  
AG PLATELET-ACTIVATING FACTOR ACETYLSHLYDROLASE  
AH DE (PAF ACETYLSHLYDROLASE) (PAF 2-ACETYLSHLYDROLASE) (EC 3.1.1.47)  
AI DE (PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYLSHLYDROLASE) (LDL-ASSOCIATED  
AJ DE ESTERASE) (1-ALKYL-2-ACETYLSHLYDROLASE) (1-ALKYL-2-ACETYLSHLYDROLASE)  
AK GN PLATg7.  
AL Canis familiaris (Dog).  
AM OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AN OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
AO XN NCBI\_TaxID=9615;  
AP [1]  
AQ SEQUENCE FROM N.A.  
AR TISSUE=Spleen;  
AS MEDLINE=96029630; PubMed=7592717;  
AT Tjoeiker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
AU RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;  
AV RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
AW RT phospholipase A2 with a catalytic triad";  
AX RL J. Biol. Chem. 270:25481-25487(1995).  
AY RL  
AZ 1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
BA CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
BB CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
BC CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
BD CC PHOSPHOLIPIDS.  
BE CC  
BF CC 1- CATALYTIC ACTIVITY: 2-ACETYLSHLYDROLASE-3-PHOSPHOLIPASE +  
BG CC H2O = 1-ALKYL-SHLYDROLASE-3-PHOSPHOLIPASE + ACETATE.  
BH CC 1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
BI CC 1- TISSUE SPECIFICITY: PLASMA.  
BJ CC 1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
BK CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
BL CC  
BM CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
BN CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
BO CC the European Bioinformatics Institute. There are no restrictions on its  
BP CC use by non-profit institutions as long as its content is in no way  
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BS CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
BT CC  
BU CC  
BV CC EMBL: U34246; AAC4848.1;  
BW CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
BX CC InterPro: IPR000734; Lipase.  
BY CC PROSITE: PS00120; LIPASE\_SER; 1.  
BZ CC Hydrolase; Lipid degradation; Glycoprotein; Signal.  
CA CC SIGNAL 1 21  
CB CC CHAIN 22 444  
CC PLATELET-ACTIVATING FACTOR  
CD CC ACETYLSHLYDROLASE  
CE CC ACT\_SITE 274 274  
CF CC CHARGE RELAY SYSTEM (BY SIMILARITY).  
CG CC ACT\_SITE 297 297  
CH CC CHARGE RELAY SYSTEM (BY SIMILARITY).  
CI CC ACT\_SITE 352 352  
CJ CC CHARGE RELAY SYSTEM (BY SIMILARITY).  
CK CC CARBOHYD 60 60  
CL CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
CM CC CARBOHYD 200 200  
CN CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
CO CC CARBOHYD 424 424  
CP CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
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SI CC  
SJ CC  
SK CC  
SL CC  
SM CC  
SN CC  
SO CC  
SP CC  
SQ CC  
SR CC  
SS CC  
ST CC  
SU CC  
SV CC  
SW CC  
SX CC  
SY CC  
SZ CC  
TA CC  
TB CC  
TC CC  
TD CC  
TE CC  
TF CC  
TG CC  
TH CC  
TI CC  
TJ CC  
TK CC  
TL CC  
TM CC  
TN CC  
TO CC  
TP CC  
TQ CC  
TR CC  
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TU CC  
TV CC  
TW CC  
TX CC  
TY CC  
TZ CC  
UA CC  
UB CC  
UC CC  
UD CC  
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UF CC  
UG CC  
UH CC  
UI CC  
UJ CC  
UK CC  
UL CC  
UM CC  
UN CC  
UO CC  
UP CC  
UQ CC  
UR CC  
US CC  
UT CC  
UU CC  
UV CC  
UW CC  
UX CC  
UY CC  
UZ CC  
VA CC  
VB CC  
VC CC  
VD CC  
VE CC  
VF CC  
VG CC  
VH CC  
VI CC  
VJ CC  
VK CC  
VL CC  
VM CC  
VN CC  
VO CC  
VP CC  
VQ CC  
VR CC  
VS CC  
VT CC  
VU CC  
VV CC  
VV CC  
VW CC  
VX CC  
VY CC  
VZ CC  
WA CC  
WB CC  
WC CC  
WD CC  
WE CC  
WF CC  
WG CC  
WH CC  
WI CC  
WJ CC  
WK CC  
WL CC  
WM

AC	Q60963:	01-NOV-1997 (Rel. 35, Created)
AD		01-NOV-1997 (Rel. 35, Last sequence update)
DE		20-NOV-2001 (Rel. 40, Last annotation update)
DE		PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE		(PAF ACETYLHYDROLASE) (PAF 2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE		PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE		ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN		PLA2G7 OR PAFAH.
GN		Mus musculus (Mouse).
OS		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI		NCBI_TaxID=10090;
ON		[1]
RP		SEQUENCE FROM N.A.
RC		TISSUE= Spleen;
RC		MEDLINE=9602630; PubMed=7592717;
RX		Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA		Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
RA		Gray P.W.;
RT		"Plasma platelet-activating factor acetylhydrolase is a secreted
RT		phospholipase A2 with a catalytic triad.";
RL		J. Biol. Chem. 270:25481-25487(1995).
CC		!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC		BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC		INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC		RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC		PHOSPHOLIPIDS.
CC		!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC		H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC		!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC		!- TISSUE SPECIFICITY: PLASMA.
CC		!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC		HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC		or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> )
CC		-----
DR	EMBL:	U34277; AAC53274.1; -;
DR	MCD:	MGI:1351327; Pla2g7.
DR	InterPro:	IPR000379; Est_lip_thioest_actsite.
DR	InterPro:	IPR000734; Lipase.
DR	PROSITE:	PS00120; LIPASE_SER: 1.
KW	Hydrolase:	Lipid degradation; Glycoprotein; Signal.
FT	SIGNAL	1 21 BY SIMILARITY.
FT	CHAIN	22 440 PLATELET-ACTIVATING FACTOR
FT		ACETYLHYDROLASE.
FT	ACT_SITE	272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CARBOHYD	59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	440 AA; 49361 MW; C82A68AD42F482EB CRC64;
Query Match 79.6%; Score 148; DB 1; Length 440;		
Best Local Similarity 80.6%; Pred. No. 8.4e-13;		
Matches 29; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
QY	2	LKLKGDSDNAIDLSNKASLAFLOKHLGHKDFDQ 37
Db	368	LTLKEIDSRVAIDLTNKSAMFLOKHLGHKDFDQ 403
RESULT	5	
ID	PAFA_CAVPO	STANDARD: PRT: 436 AA.

## RESULT 4

PAFA\_MOUSE

ID\_PAFAN

PRT; 440 AA.

ID PAFA

**STANDARD:**

PRT: 436 AA-

P07683;  
 01-NOV-1997 (Rel. 35, Created)  
 20-AUG-2001 (Rel. 40, Last sequence update)  
 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 PLA2G7 OR PAFAH.  
 Gallus gallus (Guinea pig).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10141;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=HARTLEY; TISSUE=Liver;  
 MEDLINE=97103479; PubMed=8947850;  
 Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,  
 Yokoyama K., Setaka M., Nojima S.;  
 "Cloning, expression and characterization of plasma  
 platelet-activating factor-acetylhydrolase from guinea pig.";  
 J. Biochem. 120:838-844(1996).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D67037; DAA11054.1;  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 436 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 271 271 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 436 AA; 49062 MW; C359D96E392FEE11 CRC64;  
 Query Match 72.6%; Score 135; DB 1; Length 436;  
 Best Local Similarity 75.7%; Pred. No. 5e-11; Indels 0; Gaps 0;  
 Matches 28; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Oy 1 MLKLGIDSNAAIDLSNKLASLAPLQKHLGLHKDFDQ 37  
 ||||| ||| | ||| ||||| ||||| ||||| |||||  
 Db 366 MSLKGGIDSEVMDLNKASLAPLQKYLGLDKNFQ 402  
 RESULT 6  
 ID PAF2\_CHICK STANDARD; PRT; 422 AA.  
 AC Q90678;  
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 20-AUG-2001 (Rel. 40, Last annotation update)  
 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 PLA2G7.  
 Gallus gallus (Chicken).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 Gallus.  
 NCBI\_TaxID=9031;  
 [1]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 McIntyre T.M., Stafforini D.W., Prescott S.M., Gray P.W.;  
 "Plasma platelet-activating factor acetylhydrolase is a secreted  
 phospholipase A2 with a catalytic triad.";  
 J. Biol. Chem. 270:25481-25487(1995).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U34278; AAC59717.1;  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 422 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 266 266 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 289 289 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 422 AA; 47046 MW; 15ASC794376E9141 CRC64;  
 Query Match 68.8%; Score 128; DB 1; Length 422;  
 Best Local Similarity 71.4%; Pred. No. 4.4e-10;  
 Matches 25; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 Oy 3 KLGKIDSNAAIDLSNKLASLAPLQKHLGLHKDFDQ 37  
 ||||| ||| | ||| ||||| ||||| ||||| |||||  
 Db 364 KLGKIDPNEADICNHNASLAPLQKHLGLKRDQ 398  
 RESULT 7  
 ID PAF2\_BOVIN STANDARD; PRT; 392 AA.  
 AC P79106;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC



DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).  
GN PAFH2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactylia; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=97115847; PubMed=8955149;  
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
RA Aoki J., Hattori M., Arai H., Inoue K.;  
RT "cDNA cloning and expression of intracellular platelet-activating  
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
RT acetylhydrolase.";  
RL J. Biol. Chem. 271:33032-33038(1996).  
RN [2]  
RN REVIEW  
RX MEDLINE=97364701; PubMed=9218411;  
RA Staforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
RT "Platelet-activating factor acetylhydrolases.";  
RL J. Biol. Chem. 272:17895-17898(1997).  
CC -!- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT  
CC LOWER LEVELS IN OTHER TISSUES.  
CC -!- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: D87559; BAA13419.1; -;  
CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
CC DR InterPro: IPR000734; Lipase.  
CC DR PROSITE: PS00120; LIPASE\_SER; 1.  
CC KW Hydrolase; Lipid degradation.  
CC FT ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC SO SEQUENCE 392 AA; 43865 MW; IDEACAZDFM4CEA8 CRC64;  
  
Query Match 39.2%; Score 73; DB 1; Length 392;  
Best Local Similarity 45.5%; Pred. No. 0.013;  
Matches 15; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
  
Qy 5 KGDIDSNAAIDLSNKASLAFLOKHLGHKDFDQ 37  
Db 337 RGSLDPEYEGQETVVRAMLAFLQKHLKEDYDQ 369  
  
RESULT 8  
PAF2\_HUMAN  
ID PAF2\_HUMAN STANDARD; PRT; 392 AA.  
AC Q99487; O15458;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC  
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).  
GN PAFH2.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97115847; PubMed=8955149;  
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
RA Aoki J., Hattori M., Arai H., Inoue K.;  
RT "cDNA cloning and expression of intracellular platelet-activating  
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
RT acetylhydrolase.";  
RL J. Biol. Chem. 271:33032-33038(1996).  
RN [2]  
RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.  
RC TISSUE=Prostate;  
RX MEDLINE=98161812; PubMed=9494101;  
RA Rice S.Q.J., Southern C., Boyd H.F., Terrett J.A., Macphie C.H.,  
RA Moores K., Gloger I.S., Tew D.G.;  
RT "Expression, purification and characterization of a human  
RT serine-dependent phospholipase A2 with high specificity for oxidized  
RT phospholipids and platelet activating factor.";  
RL Biochem. J. 330:1309-1315(1998).  
RN [3]  
RN REVIEW  
RX MEDLINE=97364701; PubMed=9218411;  
RA Staforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
RT "Platelet-activating factor acetylhydrolases.";  
RL J. Biol. Chem. 272:17895-17898(1997).  
CC -!- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,  
CC 3,4-DICHLOROISOCOUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DFP) AND  
CC DIETHYL P-NITROBENZYL PHOSPHATE (DENP).  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT  
CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO  
CC AMYGDALA AND FRONTAL CORTEX.  
CC -!- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.  
CC -!- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: D87845; BAA13468.1; -;  
CC DR EMBL: U89386; AAC39707.1; -;  
CC DR MIM: 602344; -;  
CC DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
CC DR InterPro: IPR000734; Lipase.  
CC DR PROSITE: PS00120; LIPASE\_SER; 1.  
CC KW Hydrolase; Lipid degradation.  
CC FT ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT CONFLICT 212 212 L -> F (IN REF. 2).  
CC SO SEQUENCE 392 AA; 44035 MW; 650FB7E6F5B68317 CRC64;  
  
Query Match 38.2%; Score 71; DB 1; Length 392;  
Best Local Similarity 42.4%; Pred. No. 0.025;  
Matches 14; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
  
Qy 5 KGDIDSNAAIDLSNKASLAFLOKHLGHKDFDQ 37  
Db 337 RGSLDPEYEGQETVVRAMLAFLQKHLKEDYDQ 369  
  
RESULT 8  
PAF2\_HUMAN  
ID PAF2\_HUMAN STANDARD; PRT; 392 AA.  
AC Q99487; O15458;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC  
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).  
GN PAFH2.  
OS Homo sapiens (Human).

RESULT 9

ID	G3P3_ECO57	STANDARD;	PRT;	333 AA.
DT	P58072;			
DT	20-AUG-2001 (Rel. 40, Created)			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DE	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	GLYERALDEHYDE 3-PHOSPHATE DEHYDROGENASE C (EC 1.2.1.12) (GAPDH-C).			
GN	GAPC OR Z2304 OR ECS2022.			
OS	Escherichia coli O157:H7.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=83334;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=O157:H7 / EDL933 / ATCC 700927;			
RC	MEDLINE=21074935; PubMed=11206551;			
RA	Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,			
RA	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,			
RA	Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,			
RA	Apodaca E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,			
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,			
RA	Welch R.A., Blattner F.R.;			
RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";			
RT	Nature 409:529-533(2001).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=O157:H7 / RIMD 0509952;			
RC	MEDLINE=21156231; PubMed=11258796;			
RX	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,			
RA	Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,			
RA	Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,			
RA	Kuhara S., Shiba T., Hattori M., Shinagawa H.;			
RT	"Complete genome sequence of enterohaemorrhagic Escherichia coli			
RT	O157:H7 and genomic comparison with a laboratory strain K-12.";			
RL	DNA Res. 8:11-22(2001).			
CC	-1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE			
CC	+ NAD(+) -> 1,3-DIPHOSPHATEGLYCERATE + NADH.			
CC	-1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.			
CC	-1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).			
CC	-1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE			
CC	DEHYDROGENASE FAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AE005364; AGS56359.1; -			
DR	EMBL; AP002557; BAB35445.1; -			
DR	PROSITE; PS00071; GAPDH. 1.			
KW	Glycolysis; Oxidoreductase; NAD; Multigene family.			
FT	BINDING 150 150			
FT	(BY SIMILARITY).			
FT	GLYCERALDEHYDE 3-PHOSPHATE			
FT	(BY SIMILARITY).			
FT	ACT_SITE 177 177			
FT	ACTIVATES THIOL GROUP DURING CATALYSIS			
FT	(BY SIMILARITY).			
SEQUENCE	333 AA; 35763 MW; A2F77CB2E773B64C CRC64;			
Query Match	28.5%; Score 53; DB 1; Length 333;			
Best Local Similarity	42.9%; Pred. No. 5.9;			
Matches 12; Conservative	7; Mismatches 9; Indels 0; Gaps 0;			
QY	1 MKLKGDTDSNAADLSNKA5LAFLOKH 28			
db	20 LLEKVSNDIVVAINDLTPKILAYLKH 47			

```

SEQUENCE OF 1-52 FROM N.A.
MEDLINE=87053179; PubMed=3780374;
RA Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;
RA "A vector-primer-cloner-sequence plasmid for the construction of cDNA
RT libraries: evidence for a rat glyceraldehyde-3-phosphate
RT dehydrogenase-like mRNA and a ferritin mRNA within testis.";
RL DNA 5:427-435(1986).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER (CYTOSOLIC).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
CC -1- CAUTION: IN THE K12 STRAIN THIS GENE IS DISRUPTED BY A STOP CODON
CC AND A FRAMESHIFT. IT SEEMS TO BE INTACT IN A NUMBER OF WILD
CC STRAINS.
CC -1- ORIGINATE. REF.8 AND REF.9 SEQUENCE WAS ORIGINALLY THOUGHT TO
CC ORIGINATE FROM RAT.
-----
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-----
EMBL; L09067; AAA23856.1; ALT_FRAME.
DR EMBL; AE000239; AAC74498.1; ALT_FRAME.
DR EMBL; AE000239; AAC74499.1; ALT_FRAME.
DR EMBL; D90780; BAA15033.1; ALT_FRAME.
DR EMBL; D90781; BAA15038.1; ALT_FRAME.
DR EMBL; M64541; ; NOT_ANNOTATED_CDS.
DR EMBL; X07569; ; NOT_ANNOTATED_CDS.
DR EMBL; X54798; CAA38569.1; -.
DR EMBL; M14166; AAA41178.1; -.
DR HSP; P17721; IHG.
DR EcoGene; EG12103; gapC.
DR InterPro; IPR000173; GAP_DH.
DR Pfam; PF00044; gpdh; 1.
DR PRINTS; PR00078; G3PDHGRNASF.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
FT BINDING 150 150
FT ACT_SITE 177 177
FT FT
FT CONFLICT 39 39 K->V (IN REF. 7 AND 8).
FT SEQUENCE 333 AA; 35649 MW; E88223297376B0A0 CRC64;
SQ
Query Match 28.5%; Score 53; DB 1; Length 333;
Best Local Similarity 42.9%; Pred.No.5,9;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MLKLKGDIDSNAAIDLSNKASLAFLQKH 28
DB 20 LLEVKNSIDVVAINDLTPKILAYLLKH 47
:::| | | | | | | | | | | | | | | |
RESULT 11
CSKI_SCHPO STANDARD; PRT; 306 AA.
AC P36615;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTEIN KINASE CSK1 (EC 2.7.1.-).
GN CSK1 OR SPAC14.06C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

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OC Schizosaccharomyces.
NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
MEDLINE=93223713; PubMed=8467814;
Molz L., Beach D.;
RT "Characterization of the fission yeast mcs2 cyclin and its associated
protein kinase activity.";
EMBO J. 12:1723-1732(1993).
[2]
RN
RC SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN. COULD FUNCTION IN ASSOCIATION WITH CYCLIN
CC MCS2.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDC2X SUBFAMILY.
CC -----
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CC -----
DR EMBL; S59896; AAB26194.1; -.
DR EMBL; Z69239; CAAG3215.1; -.
DR PIR; S39151; S39151.
DR HSSP; P24941; IAQI.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00069; Pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transfaser; Serine/threonine-protein kinase; ATP-binding.
FW DOMAIN 11 306
FT NP_BIND 17 25 ATP (BY SIMILARITY).
FT BINDING 40 40 ATP (BY SIMILARITY).
FT ACT_SITE 129 129 BY SIMILARITY.
SQ SEQUENCE 306 AA; 34672 MW; E670D87547523D0C CRC64;

Query Match 27.4%; Score 51; DB 1; Length 306;
Best Local Similarity 40.7%; Pred. No. 10;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 IDSNAAIDLNSKASLAFLQKHGLHGD 34
||| ||| :||| :||| |||
Db 103 IDTKCKIVLOISSALEYLEKHGILHRD 129

RESULT 12
FEMA_STAATU
ID FEMA_STAATU STANDARD; PRT; 433 AA.
AC P14304;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE FACTOR ESSENTIAL FOR EXPRESSION OF METHICILLIN RESISTANCE.
FM FMA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RX [1]
RP SEQUENCE FROM N.A.
RM MEDLINE=90136516; PubMed=2559314;
RA Berger-Bachli B., Barberis-Maino L., Straessle A., Kayser F.H.;
RA "Fema", a host-mediated factor essential for methicillin resistance in
RT Staphylococcus aureus: molecular cloning and characterization.";

```

RL Mol. Genet. 219:263-269(1989).  
CC -1- FUNCTION: FEMA MAY BE INVOLVED IN CELL WALL OR MEMBRANE  
CC METABOLISM, OR IT MIGHT BE A CONTROL ELEMENT ACTING ON EXPRESSION  
CC OF GENES INVOLVED IN CELL WALL OR MEMBRANE BIOSYNTHESIS.  
CC -1- MISCELLANEOUS: INVOLVED IN RESISTANCE TO THE ANTIBIOTIC  
CC METHICILLIN.  
CC -1- SIMILARITY: WITH ORF419 (FEMB).  
CC  
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CC  
CC EMBL; X17688; CAA35679.1; .  
DR PIR; S06783; S06783.  
DR InterPro; IPR003447; FemAB.  
DR Pfam; PF02388; FemAB; 1.  
KW Antibiotic resistance.  
SQ SEQUENCE 433 AA; 50650 MW; 4388E2BDF01573CB CRC64;  
  
Query Match 27.4%; Score 51; DB 1; Length 433;  
Best Local Similarity 39.4%; Pred. No. 15;  
Matches 13; Conservative 4; Mismatches 12; Indels 4; Gaps 2;  
  
QY 6 GDIDNSNAID--LSNKASLAFLOKHLGLHKDFD 36  
I: ||| | : : : : : ||| ||  
D 133 GEITGNAGNDWFEKMSNLGF--EHTGFHKGF 163  
  
RESULT 13  
CRAC\_DICDI  
ID CRAC\_DICDI STANDARD; PRT; 597 AA.  
AC P33401;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE DICTYOSTELIUM.  
DE PROTEIN CRAC.  
GN DAGA.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=AX4;  
RA MEDLINE=94375528; PubMed=8089184;  
RA Insall R., Kupsa A., Lilly P.J., Shaulsky G., Levin L.R., Loomis W.F.,  
RA Devreotes P.N.;  
RA "CRAC, a cytosolic protein containing a pleckstrin homology domain,  
RT is required for receptor and G protein-mediated activation of  
RT adenylyl cyclase in Dictyostelium.";  
RL J. Cell Biol. 126:1537-1545(1994).  
RN [2]  
RP SEQUENCE OF 1-8.  
RX MEDLINE=94245733; PubMed=8188693;  
RA Lilly P.J., Devreotes P.N.;  
RA "Identification of CRAC, a cytosolic regulator required for guanine  
RT nucleotide stimulation of adenylyl cyclase in Dictyostelium.";  
RL J. Biol. Chem. 269:14123-14129(1994).  
CC -1- FUNCTION: COUPLES ACTIVATED G PROTEIN TO ADENYLYL CYCLASE SIGNAL  
CC TRANSDUCTION FROM SURFACE CAMP RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- DEVELOPMENTAL STAGE: TIGHTLY DEVELOPMENTALLY REGULATED.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
CC  
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CC  
CC EMBL; U06228; AAA61782.1; .  
DR PIR; A54796; A54796.  
DR DictyDB; D002034; dagA.  
DR InterPro; IPR001849; PH.  
DR Pfam; PF00169; PH; 1.  
DR SMART; SM00233; PH; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
FT INIT\_MET 0  
FT DOMAIN 21 121 PH.  
FT DOMAIN 349 362 POLY-THR.  
FT DOMAIN 467 479 POLY-GLY.  
FT DOMAIN 612 623 POLY-SER.  
SQ SEQUENCE 697 AA; 78399 MW; 4B0B41AF313DEDC7 CRC64;  
  
Query Match 27.4%; Score 51; DB 1; Length 697;  
Best Local Similarity 24.2%; Pred. No. 25;  
Matches 8; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
  
QY 3 KIKGDIDNSNAIDLSNKASLAFLOKHLGLHKDF 35  
I: ||| | : : : : : ||| :  
D 17 KIKGDVSYSSIMKKAGNGKGFLEDFYFALHRY 49  
  
RESULT 14  
METK\_RAT  
ID METK\_RAT STANDARD; PRT; 395 AA.  
AC P18298;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE GAMMA FORM (EC 2.5.1.6) (METHIONINE  
DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) (MAT-II).  
GN MAT2A OR AMS2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=Kidney;  
RX MEDLINE=90337979; PubMed=1696256;  
RA Horikawa S., Sasuga J., Shimizu K., Ozasa H., Tsukada K.;  
RT "Molecular cloning and nucleotide sequence of cDNA encoding the rat  
RT kidney S-adenosylmethionine synthetase.";  
RL J. Biol. Chem. 265:13683-13686(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hiroki T., Horikawa S., Tsukada K.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC METHIONINE AND ATP.  
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +  
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.  
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT  
CC FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA  
CC AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY  
CC DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM  
CC PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY  
CC REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
CC  
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```
CC -----
CC EMBL; J05571; AAA42106.1; -.
DR EMBL; AB000717; BAA19170.1; -.
DR EMBL; AB000716; BAA19170.1; JOINED.
DR PIR; A37118; A37118.
DR HSP; P04384; IXRC.
DR InterPro; IPR002133; S-AdoMet_synt.
DR Pfam; PF00438; S-AdoMet_synt; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 131 136
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43715 MW; 4DA9AFABF7D09C79 CRC64;
```

Query Match 27.2%; Score 50.5; DB 1; Length 395;  
Best Local Similarity 41.0%; Pred. No. 16;  
Matches 16; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

```
QY 1 MLKLGDDTSNAAIDLSNKASIAFLQKHLGL---HKDPD 36
   | | | | | | | | | | | | | | | | | |
DB 64 MILLAGETTSRAAIDYQKVREAI--KHIGYDDSSKGF 100
```

```
RESULT 15
SP21_YEAST
ID SP21_YEAST STANDARD; PRT; 758 AA.
AC P35209;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE SPT21 PROTEIN.
GN SPT21 OR YMR179W OR YMR8010.09.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94186069; PubMed=8138180;
RA Natsoulis G., Winston F., Boeke J.D.;
RT "The SPT10 and SPT21 genes of Saccharomyces cerevisiae.";
RL Genetics 136:93-105(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR NORMAL TRANSCRIPTION AT A NUMBER OF LOCI IN
CC YEAST.
CC -----
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```
CC -----
CC EMBL; L24436; AAA35078.1; -.
DR EMBL; Z49808; CAA89912.1; -.
DR PIR; S47866; S47866.
DR SGD; S0004791; SPT21.
FT DOMAIN 127 144 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 672 682 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 758 AA; 84697 MW; 7DB3FCF7EE996705 CRC64;
```



Query Match 27.2%; Score 50.5; DB 1; Length 758;  
Best Local Similarity 32.4%; Pred. No. 32;  
Matches 11; Conservative 10; Mismatches 12; Indels 1; Gaps 1;


```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:33:04 ; Search time 94.88 Seconds  
(without alignments)  
57.041 Million cell updates/sec

```

Title: US-09-922-067-1
Perfect score: 186
Sequence: 1 MLKLGKIDISNAIDLSNKASLAFLOKHGLGLHKDEDO 37

```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

```
Database :
SPREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
1	57	30.6	418	2	Q9X6T1	Q9X6T1	staphylococ
2	57	30.6	430	4	Q9HB15	Q9HB15	homo sapien
3	57	30.6	430	11	Q9ERS1	Q9ERS1	rattus norv
4	56	30.1	803	2	Q9ED70	Q9ED70	enterococu
5	54	29.0	408	4	Q9HB14	Q9HB14	homo sapien
6	54	29.0	1089	9	Q9MCS3	Q9MCS3	bacterioph
7	54	29.0	1516	4	Q9C0D2	Q9C0D2	homo sapien
8	53.5	28.8	136	2	Q9AI05	Q9AI05	photorhabd
9	53	28.5	56	2	Q9Y487	Q9Y487	caedibacter
10	53	28.5	111	2	Q9K5J8	Q9K5J8	bacillus an
11	53	28.5	238	9	Q9MBT8	Q9MBT8	staphylococ
12	53	28.5	348	9	Q38045	Q38045	bacterioph
13	53	28.5	736	10	O80440	O80440	arabidopsis
14	53	28.5	1032	2	Q9KYL1	Q9KYL1	streptomyce
15	52.5	28.2	755	4	Q9UFE4	Q9UFE4	homo sapien
16	52	28.0	211	2	Q9AHD1	Q9AHD1	streptococc
17	52	28.0	422	2	F95734	F95734	staphylococ
18	52	28.0	803	1	Q9C424	Q9C424	methanocarc
19	51	27.4	420	2	Q99UA7	Q99UA7	staphylococ

## ALIGNMENTS

RESULT	1
ID	Q9X6T1
AC	PRELIMINARY;
CD	PRT; 418 AA.
DT	01-NOV-1999 (TREMBRel. 12, Created)
DR	01-NOV-1999 (TREMBRel. 12, Last sequence update)
DE	01-JUN-2001 (TREMBRel. 17, Last annotation update)
GN	FACTORY ESSENTIAL FOR METHICILLIN RESISTANCE.
OS	FEMA.
OC	Staphylococcus warneri.
CC	Bacteria; Firmicutes; Bacillus/Clostridium group;
CX	Bacillus/Staphylococcus group; Staphylococcus.
RN	NCBI_TaxID=1292;
RT	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 20316;
RD	Vannuffel P., Heusterspreute M., Gala J.-L.;
RT	"Cloning and characterization of femA genes from Staphyl-
RL	species.";
RR	BL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF144663; AAD33942.1; --
DR	InterPro: IPR003447; FemAB.
DR	Pfam: PF02388; FemAB; 1
SQ	SEQUENCE 418 AA: 48703 MW: 62EAF6DE50C5596 CRC64;
OY	6 GDIDSNAID--LSNKASLAFLKHLGLHKDFD 36 
Db	120 GDIITAGNDWTFDKLASLGf--KHGFGHNGFD 150
RESULT	2
Q9HB15	
ID	Q9HB15
AC	PRELIMINARY;
CD	PRT; 430 AA.
DT	01-MAR-2001 (TREMBRel. 16, Created)
DR	01-MAR-2001 (TREMBRel. 16, Last sequence update)
DE	01-JUN-2001 (TREMBRel. 17, Last annotation update)

```
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-2.
GN KCNK12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rajan S., Derst C.;
RT "Cloning and sequencing of two novel tandem pore domain potassium
RT channels."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF287302; AAG32313.1; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2POREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 430 AA; 46888 MW; 7D6DC7C3789277FF CRC64;

Query Match 30.6%; Score 57; DB 4; Length 430;
Best Local Similarity 48.1%; Pred. No. 7;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 KLGKGDIDNSNAIDLSNKSALFLQKHL 29
Db 363 RLSGELISMRLDTASNKVSLALQKQL 389

RESULT 3
QYERS1 PRELIMINARY; PRT; 430 AA.
AC Q9ERS1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-2.
GN KCNK12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WISTAR; TISSUE=BRAIN;
RA Rajan S., Derst C.;
RT "Cloning and sequencing of two novel tandem pore domain potassium
RT channels."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF287300; AAG32311.1; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2POREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 430 AA; 46964 MW; 69F1D16C6BFE7180 CRC64;

Query Match 30.6%; Score 57; DB 11; Length 430;
Best Local Similarity 48.1%; Pred. No. 7;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 3 KLGKGDIDNSNAIDLSNKSALFLQKHL 29
Db 363 RLSGELISMRLDTASNKVSLALQKQL 389

RESULT 4
QYERS1 PRELIMINARY; PRT; 803 AA.
AC Q9ERS1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-2.
GN KCNK12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WISTAR; TISSUE=BRAIN;
RA Rajan S., Derst C.;
RT "Cloning and sequencing of two novel tandem pore domain potassium
RT channels."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF287300; AAG32311.1; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2POREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 430 AA; 46964 MW; 69F1D16C6BFE7180 CRC64;
```

```
DE ACETYL-COA ACETYLTRANSFERASE/HMG-COA REDUCTASE.
GN MVAE.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20353468; PubMed=10894743;
RA Wilding E.I., Brown J.R., Bryant A.P., Chaliker A.F., Holmes D.J.,
RA Ingraham K.A., Iordanescu S., So C.Y., Rosenberg M., Gwynn M.N.;
RT "Identification, evolution and essentiality of the mevalonate pathway
RT for isopentenyl diphosphate biosynthesis in gram-positive cocci."
RL J. Bacteriol. 182:4319-4327(2000).
DR EMBL; AF290092; AAG02439.1; -.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR002155; Thiolase.
DR Pfam; PF00368; HMG-CoA_red; 1.
DR Pfam; PF00108; thiolase; 1.
DR PRINTS; PR00071; HMGCOARDTASE.
DR PROSITE; PS00065; HMG-COA_REDUCTASE_4; 1.
DR PROSITE; PS00098; THIOLASE_1; 1.
KW Transferase.
SQ SEQUENCE 803 AA; 86496 MW; F3678A6EAAA43FC0 CRC64;

Query Match 30.1%; Score 56; DB 2; Length 803;
Best Local Similarity 28.6%; Pred. No. 20;
Matches 10; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 3 KLGKGDIDNSNAIDLSNKSALFLQKHLGRHDFQ 37
Db 16 KYKGLSLOVSAVDLGTHTVTTLLKRHSITSEIDQ 50

RESULT 5
QYHBI4 PRELIMINARY; PRT; 408 AA.
AC Q9HBI4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-1.
GN KCNK13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rajan S., Derst C.;
RT "Cloning and sequencing of two novel tandem pore domain potassium
RT channels."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF287303; AAG32314.1; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2POREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 408 AA; 45392 MW; B7E3CA1AFD59E419 CRC64;

Query Match 29.0%; Score 54; DB 4; Length 408;
Best Local Similarity 48.1%; Pred. No. 18;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 KLGKGDIDNSNAIDLSNKSALFLQKHL 29
Db 341 RLSGELISMRLDTASNKVSLALQKQL 367

RESULT 6
QYHBI4 PRELIMINARY; PRT; 408 AA.
AC Q9HBI4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-1.
GN KCNK13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rajan S., Derst C.;
RT "Cloning and sequencing of two novel tandem pore domain potassium
RT channels."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF287303; AAG32314.1; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2POREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 408 AA; 45392 MW; B7E3CA1AFD59E419 CRC64;
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**[T] NY**

RC STRAIN=A3(2);  
RA Saunders D.C.; HRC STRAIN=A3(2);  
RA Saunders D.C.; H

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RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RP [2]
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL356593; CAB92219.1;
KW Hypothetical protein.
SQ SEQUENCE 1032 AA; 113651 MW; 4EF959B8BCDEF21 CRC64;

Query Match 28.5%; Score 53; DB 2; Length 1032;
Best Local Similarity 44.0%; Pred. No. 70;
Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 9 DSNRAIDLSNKASLAFLOKHLGLHK 33
DB 685 DOLLPLDLSERAHLALRAHLDTHE 709

RESULT 15
Q9UFE4 PRELIMINARY; PRT; 755 AA.
ID Q9UFE4
AC Q9UFE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HYPOTHETICAL 88.2 KDA PROTEIN.
GN DKFZP434A128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL122120; CAB59277.1;
KW Hypothetical protein.
SQ SEQUENCE 755 AA; 88230 MW; B971EE2F7E0F958B CRC64;

Query Match 28.2%; Score 52.5; DB 4; Length 755;
Best Local Similarity 28.6%; Pred. No. 58;
Matches 14; Conservative 10; Mismatches 12; Indels 13; Gaps 2;

QY 1 MLKLGKGDIDSNAAIDLSN-----KASLAFLOKHLGLHKDFDQ 37
DB 318 MOKRGDID-NCALRLARIKQETREKENLYKEIKFLEISEIGNNTEFEK 365

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Search completed: March 9, 2002, 00:46:48  
 Job time: 824 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:56 ; Search time 114.5 Seconds  
(without alignments)  
19.408 Million cell updates/sec

Title: us-09-922-067-2

Perfect score: 170

Sequence: 1 WMFLGDEVYSRIPQLFFINSEYQYPAN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	440	22	Mouse-Human plasma
2	170	100.0	440	22	Mouse-Human plasma
3	170	100.0	441	16	Human acetyl hydro
4	170	100.0	441	16	Human acetyl hydro
5	170	100.0	441	16	Human acetyl hydro
6	170	100.0	441	16	Human acetyl hydro
7	170	100.0	441	16	Human acetyl hydro
8	170	100.0	441	16	Human acetyl hydro
9	170	100.0	441	16	Human acetyl hydro
10	170	100.0	441	16	Human acetyl hydro
11	170	100.0	441	16	Human acetyl hydro

12	170	100.0	441	16	AA73046	Human acetyl hydro
13	170	100.0	441	16	AA73047	Human acetyl hydro
14	170	100.0	441	16	AA71913	Human plasma plate
15	170	100.0	441	18	AAW26498	Human platelet-act
16	170	100.0	441	18	AAW23796	Human plasma plate
17	170	100.0	441	18	AAW09808	Platelet-activatin
18	170	100.0	441	19	AAW38361	Human plasma plate
19	170	100.0	441	20	AAW96334	Human plasma plate
20	170	100.0	441	20	AAW73359	Human PAF-AH prote
21	170	100.0	441	21	AAW7774	Plasma platelet-ac
22	170	100.0	441	21	AAW01942	Human low density
23	170	100.0	441	21	AAW8301	Human platelet-act
24	170	100.0	441	21	AAW50735	Human PAF-AH prote
25	170	100.0	441	22	AAE00761	Human plasma plate
26	170	100.0	441	22	AAE00768	Human plasma plate
27	170	100.0	441	22	AAE00769	Human plasma plate
28	170	100.0	441	22	AAE00770	Human plasma plate
29	170	100.0	441	22	AAE00771	Human plasma plate
30	170	100.0	441	22	AAE00772	Human plasma plate
31	170	100.0	441	22	AAE00774	Human plasma plate
32	170	100.0	441	22	AAE00775	Human plasma plate
33	170	100.0	441	22	AAE00776	Human platelet-act
34	170	100.0	441	22	AAE00777	Human plasma plate
35	170	100.0	441	22	AAE00778	Human plasma plate
36	170	100.0	441	22	AAE00779	Human plasma plate
37	170	100.0	441	22	AAE00780	Human plasma plate
38	170	100.0	441	22	AAE00781	Human plasma plate
39	170	100.0	441	22	AAW49451	Platelet-activatin
40	170	100.0	442	16	AAW49428	Human T-cell lymph
41	162	95.3	441	22	AAE00773	Human plasma plate
42	155	91.2	444	18	AAW26502	Bovine platelet-ac
43	155	91.2	444	20	AAW96337	Bovine plasma plat
44	155	91.2	444	20	AAW73362	Bovine PAF-AH prot
45	155	91.2	444	21	AAW07920	A bovine platelet-

#### ALIGNMENTS

RESULT 1

AAE00782

ID AAE00782 standard; Protein; 440 AA.

XX AAE00782;

XX 02-JUL-2001 (first entry)

XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC1.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
antiflammatory; septicaemia; inflammation; haemostasis; parturition;  
asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..97  
FT /note= "Corresponds to N-terminal 97 amino acids of mouse  
plasma platelet-activating factor acetylhydrolase  
(PAF-AH)"  
FT 98..440

FT Region  
FT /note= "Corresponds to C-terminal 343 amino acids of  
human plasma platelet-activating factor acetylhydrolase  
(PAF-AH)"

US6203790-B1.

20-MAR-2001.

23-MAY-2000; 2000US-0577758.

07-JUN-1995; 95US-0480658.

PR 22-JAN-1998; 98US-0010715.  
 PR 06-OCT-1993; 93US-0133803.  
 PR 06-OCT-1994; 94US-0318905.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 2001-280610/29.  
 DR N-PSDB; AAD04168.  
 XX  
 PT Treating a mammal susceptible to or suffering from septicemia comprises  
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
 PT supplement endogenous PAF-AH activity and to inactivate pathological  
 PT amounts of PAF -  
 XX  
 PS Example 8; Column -: 54pp; English.  
 XX  
 CC The present sequence is mouse-human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid  
 CC pRC/PH.MHC1.  
 CC The invention relates to human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
 CC invention also relates to method of treating a mammal susceptible to  
 CC or suffering from septicemia. PAF functions in normal physiological  
 CC processes such as inflammation, haemostasis and parturition. PAF-AH  
 CC specific antibodies are used in the diagnostic methods to detect abnormal  
 CC levels of PAF-AH in serum and also for treating the pathological  
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
 CC shock and arthritis. PAF-AH antibody is also useful for screening a  
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting  
 CC in replacement of amino acid Val to Phe at position 279. Thus the  
 CC deficiency of PAF-AH activity is due to the genetic lesion in human  
 CC plasma PAF-AH gene.  
 XX  
 SQ Sequence 440 AA;  
 Query Match 100.0%; Score 170; DB 22; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30  
 |||||  
 Db 297 wmfplgdevysripqplffinseyfqpypan 326  
 RESULT 2  
 ID AAE00783  
 XX AAE00783 standard; Protein; 440 AA.  
 AC AAE00783;  
 XX  
 DT 02-JUL-2001 (first entry)  
 XX  
 DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.  
 XX  
 KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
 KW antinflammatory; septicemia; inflammation; haemostasis; parturition;  
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 XX 1..40  
 FT Region /note- "Corresponds to N-terminal 40 amino acids of mouse  
 FT plasma platelet-activating factor acetylhydrolase  
 FT (PAF-AH)"  
 FT 41..440  
 FT Region /note- "Corresponds to C-terminal 400 amino acids of

FT human plasma platelet-activating factor acetylhydrolase  
 FT (PAF-AH)\*  
 XX  
 PN US6203790-B1.  
 XX  
 PD 20-MAR-2001.  
 XX  
 PF 23-MAY-2000; 2000US-0577758.  
 XX  
 XX 07-JUN-1995; 95US-0480658.  
 PR 22-JAN-1998; 98US-0010715.  
 PR 06-OCT-1993; 93US-0133803.  
 PR 06-OCT-1994; 94US-0318905.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 2001-280610/29.  
 DR N-PSDB; AAD04169.  
 XX  
 PT Treating a mammal susceptible to or suffering from septicemia comprises  
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
 PT supplement endogenous PAF-AH activity and to inactivate pathological  
 PT amounts of PAF -  
 XX  
 PS Example 8; Column -: 54pp; English.  
 XX  
 CC The present sequence is mouse-human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid  
 CC pRC/PH.MHC2.  
 CC The invention relates to human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
 CC invention also relates to method of treating a mammal susceptible to  
 CC or suffering from septicemia. PAF functions in normal physiological  
 CC processes such as inflammation, haemostasis and parturition. PAF-AH  
 CC specific antibodies are used in the diagnostic methods to detect abnormal  
 CC levels of PAF-AH in serum and also for treating the pathological  
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
 CC shock and arthritis. PAF-AH antibody is also useful for screening a  
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting  
 CC in replacement of amino acid Val to Phe at position 279. Thus the  
 CC deficiency of PAF-AH activity is due to the genetic lesion in human  
 CC plasma PAF-AH gene.  
 XX  
 SQ Sequence 440 AA;  
 Query Match 100.0%; Score 170; DB 22; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30  
 |||||  
 Db 297 wmfplgdevysripqplffinseyfqpypan 326  
 RESULT 3  
 ID AAR73048  
 XX AAR73048 standard; Protein; 441 AA.  
 AC AAR73048;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant C291S.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.

```

XX FH Key Location/Qualifiers
XX FT Misc-difference 291
XX FT /note= "Wild-type Cys is substd. by Ser."
XX XX
XX PN WO9509921-A.
XX PD 13-APR-1995.
XX XX
XX PF 06-OCT-1994; 94WO-US11340.
XX XX
XX PR 06-OCT-1993; 93US-0133803.
XX XX
XX PA (ICOS-) ICOS CORP.
XX XX
XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX XX
XX DR WPI; 1995-155262/20.
XX XX
XX PT New nucleic acid encoding platelet activating factor,
XX PT acetylhydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX XX
XX PS Example 10; ; 88pp; English.
XX XX
XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
Db ||||||||||||||||||||||||||||
298 wmfplgdevysripqplffinsefygypan 327

RESULT 4
AAR73049
ID AAR73049 standard; Protein; 441 AA.
XX AC AAR73049;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE Human acetyl hydrolase (AH) mutant C334S.
XX XX
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 334
XX FT /note= "Wild-type Cys is substd. by Ser."
XX XX
XX PN WO9509921-A.
XX PD 13-APR-1995.
XX XX
XX PF 06-OCT-1994; 94WO-US11340.

```

```

XX XX
XX PR 06-OCT-1993; 93US-0133803.
XX PA (ICOS-) ICOS CORP.
XX XX
XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX XX
XX DR WPI; 1995-155262/20.
XX XX
XX PT New nucleic acid encoding platelet activating factor,
XX PT acetylhydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX XX
XX PS Example 10; ; 88pp; English.
XX XX
XX CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
Db ||||||||||||||||||||||||||||
298 wmfplgdevysripqplffinsefygypan 327

RESULT 5
AAR73050
ID AAR73050 standard; Protein; 441 AA.
XX AC AAR73050;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE Human acetyl hydrolase (AH) mutant C407S.
XX XX
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 407
XX FT /note= "Wild-type Cys is substd. by Ser."
XX XX
XX PN WO9509921-A.
XX XX
XX PD 13-APR-1995.
XX XX
XX PF 06-OCT-1994; 94WO-US11340.
XX XX
XX PR 06-OCT-1993; 93US-0133803.
XX XX
XX PA (ICOS-) ICOS CORP.
XX XX
XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX XX
XX DR WPI; 1995-155262/20.
XX XX

```

PT New nucleic acid encoding platelet activating factor,  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
 DQ 298 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 327

RESULT 6

AAR71920  
 ID AAR71920 standard; Protein; 441 AA.

XX AAR71920;

DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S108A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given

CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
 DQ 298 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 327

RESULT 7

AAR71921  
 ID AAR71921 standard; Protein; 441 AA.

XX AAR71921;

DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S273A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;



Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
 |||||  
 Db 298 wmfplgdevysripqplffinseyfgypan 327

## RESULT 8

AAR71922  
 ID AAR71922 standard; Protein; 441 AA.

XX AC AAR71922;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D296A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 296 /note= "Wild-type Asp is substd. by Ala."

XX PN WO9509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
 |||||  
 Db 298 wmfplgdevysripqplffinseyfgypan 327

## RESULT 9

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

AAR71923  
 ID AAR71923 standard; Protein; 441 AA.

XX AC AAR71923;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D338A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 338 /note= "Wild-type Asp is substd. by Ala."

XX PN WO9509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
 |||||  
 Db 298 wmfplgdevysripqplffinseyfgypan 327

## RESULT 10

AAR71924  
 ID AAR71924 standard; Protein; 441 AA.

XX AC AAR71924;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant H351A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 351

FT /note= "Wild-type His is substd. by Ala."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX PL Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,

XX acetylhydrolase - useful in diagnosis and for treating

XX inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WMFPLGDEVYSRIPOPLFFINSEYFYQYpan 30

Db 298 wmfplgdevysripqplffinsefyqypan 327

RESULT 11

AAR71925

ID AAR71925 standard; Protein; 441 AA.

AC AAR71925;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant H395A/H399A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX Misc-difference 395

XX /note= "Wild-type His is substd. by Ala."

XX 399

XX /note= "Wild-type His is substd. by Ala."

XX PA

XX

PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX PL Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,

XX acetylhydrolase - useful in diagnosis and for treating

XX inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WMFPLGDEVYSRIPOPLFFINSEYFYQYpan 30

Db 298 wmfplgdevysripqplffinsefyqypan 327

RESULT 12

AAR73046

ID AAR73046 standard; Protein; 441 AA.

AC AAR73046;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C67s.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX Misc-difference 67

XX /note= "Wild-type Cys is substd. by Ser."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX

PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 DR WPI; 1995-155262/20.  
 XX  
 XX New nucleic acid encoding platelet activating factor.  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 XX Example 10; ; 88pp; English.  
 XX  
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
 |||||  
 Db 298 wmfplgdevysripqlffinseyfgypan 327

RESULT 13  
 AAR73047  
 ID AAR73047 standard; Protein; 441 AA.  
 AC AAR73047;  
 XX  
 XX 06-DEC-1995 (first entry)  
 DT  
 XX Human acetyl hydrolase (AH) mutant C229S.  
 DE  
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 229 /note= "Wild-type Cys is substd. by Ser."  
 FT  
 FT W09509921-A.  
 PN  
 XX 13-APR-1995.  
 PD  
 XX 06-OCT-1994; 94WO-US11340.  
 PF  
 XX 06-OCT-1993; 93US-0133803.  
 PR  
 XX (ICOS-) ICOS CORP.  
 PA  
 XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX WPI; 1995-155262/20.  
 XX  
 XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 XX Example 10; ; 88pp; English.

XX  
 CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
 |||||  
 Db 298 wmfplgdevysripqlffinseyfgypan 327

RESULT 14  
 AAR71913  
 ID AAR71913 standard; Protein; 441 AA.  
 XX  
 XX AAR71913;  
 AC  
 XX 05-DEC-1995 (first entry)  
 DT  
 XX Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).  
 DE  
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W09509921-A.  
 PN  
 XX 13-APR-1995.  
 PD  
 XX 06-OCT-1994; 94WO-US11340.  
 PF  
 XX 06-OCT-1993; 93US-0133803.  
 PR  
 XX (ICOS-) ICOS CORP.  
 PA  
 XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX WPI; 1995-155262/20.  
 DR  
 DR N-PSDB; AAQ87947.  
 XX  
 XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 XX Claim 5; Page 53-54; 88pp; English.

XX  
 CC The human acetyl hydrolase gene (AAQ87947) has been isolated and  
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913)  
 CC is useful in the treatment of inflammatory diseases, in particular  
 CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in  
 CC raising monoclonal antibodies specific for PAF-AH that are useful in  
 CC the diagnosis of such diseases.  
 XX  
 XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;

1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30  
298 wmfplgdevysripqplffinsevfqypan 327







```
Query Match      100.0%; Score 170; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 30; Conservative 0; Mismatches 0; Indels
```

Qy	1	WNFPLGDEVYSRIPQPLFFINSEYFQY	30
Db	1	WNFPLGDEVYSRIPQPLFFINSEYFQY	30

## RESULT 2

```

US-08-387-858A-2
: Sequence 2, Application US/08387858A
: Patent No. 5981252
: GENERAL INFORMATION:
: APPLICANT: MacPhee, Colin Houston
: APPLICANT: Tew, David Graham
: APPLICANT: Southan, Christopher Donald
: APPLICANT: Hickey, Dierdre Mary Bernadette
: APPLICANT: Glozier, Israel Simon
: APPLICANT: Lawrence, Geoffrey Mark Prouse
: APPLICANT: Rice, Simon Quintyn John
: TITLE OF INVENTION: Compounds
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406

```

```

;
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;

```

[illegible]

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/01374  
FILING DATE: 24 June 1994

ATTORNEY/AGENT INFORMATION:

NAME: Dustman, Wayne J.

NAME: DUSCULL, WAYNE J.  
REGISTRATION NUMBER: 33 970

REGISTRATION NUMBER: 33,870

REFERENCE/DOCKET NUMBER: P3

TELECOMMUNICATION INFORMATION

TELEPHONE: 610-270-5023

TELEFAX: 610-270-5090

TELEX:

: INFORMATION FOR SEQ ID NO:

INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

LENGTH: 30 amino acids

TYPE: amino acid

TOPLOGY: linear

; MOLECULE TYPE: peptide

HYPOTHETICAL: NO

```

: FRAGMENT TYPE: internal

```

US-08-387-858A-2 INTERNAL

US-08-387-858A-2

Query Match 100.0%; Score 170; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.5e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels

1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

### RESULT 3

```

US-09-294-384B-2
: Sequence 2, Application US/09294384B
: Patent No. 6177257
: GENERAL INFORMATION:
: APPLICANT: MacPhee, Colin Houston
: APPLICANT: Tew, David Graham
: APPLICANT: Southan, Christopher Donald
: APPLICANT: Hickey, Dierdre Mary Bernadette
: APPLICANT: Gloger, Israel Simon
: APPLICANT: Lawrence, Geoffrey Mark Prouse
: APPLICANT: Rice, Simon Quentyn John
: TITLE OF INVENTION: Compounds
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EP0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/294,384B
: FILING DATE:

```

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,858  
FILING DATE: 24 February 1995  
APPLICATION NUMBER: PCT/GB94/01374  
FILING DATE: 24 June 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090

TELEFAX: 010-270-3030  
TELEX:

```

1 INDEX:
2 INFORMATION FOR SEQ ID NO: 2:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 30 amino acids
5 TYPE: amino acids
6 TOPOLOGY: linear
7 MOLECULE TYPE: peptide
8 HYPOTHETICAL: NO
9 FRAGMENT TYPE: internal
10 US-00-294-1848-2

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Query Match 100.0%; Score 170; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.5e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30  
db 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30

## RESULTS

US-08-470-187-8  
Sequence 8, Application US/08470187  
Patent No. 5532152  
GENERAL INFORMATION:  
APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine E.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Receptor



```

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/318,905
  FILING DATE:
  CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/133,803
    FILING DATE: 6-OCT-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Ng, 5641669and, Greta E.
    REGISTRATION NUMBER: 35,302
  REFERENCE/DOCKET NUMBER: 32205
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (312) 474-6300
    TELEFAX: (312) 474-0448
    TELEX: 25-3658
  INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 441 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-08-318-905-8

Query Match          100.0%; Score 170; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels

QY      1  WMFPLGDEVYSRIPQPLFFINSEYFYQPAN 30
        |||||
DB      298 WMFPLGDEVYSRIPQPLFFINSEYFYQPAN 327

RESULT# 6
US-08-483-232-8
  Sequence 8, Application US/08483232
  Patent No. 5656431
  GENERAL INFORMATION:
    APPLICANT: Cousins, Lawrence S.
    APPLICANT: Eberhardt, Christine D.
    APPLICANT: Gray, Patrick W.
    APPLICANT: Le Trong, Hai
    APPLICANT: Tjoelker, Larry W.
    APPLICANT: Wilder, Cheryl L.
  TITLE OF INVENTION: Platelet-Activating Factor
  NUMBER OF SEQUENCES: 30
  CORRESPONDENCE ADDRESS:
    ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
    STREET: 6300 Sears Tower, 233 South Wacker Drive
    CITY: Chicago
    STATE: Illinois
    COUNTRY: United States of America
    ZIP: 60606-6402
  COMPUTER READABLE FORM:
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentID Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/483,232
    FILING DATE:
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/318,905
    FILING DATE: 06-OCT-1994
  PRIOR APPLICATION NUMBER: US 08/133,803
  FILING DATE: 06-OCT-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Ng, 565643land, Greta E.
    REGISTRATION NUMBER: 35,302
    REFERENCE/DOCKET NUMBER: 27866/32689

```

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-232-8

Query Match 100.0%; Score 170; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
DB 298 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 327

## RESULT 7

US-08-483-140-8  
Sequence 8, Application US/08483140  
Patent No. 5698403  
GENERAL INFORMATION:

APPLICANT: ICOS Corporation  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,140  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 6-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5698403and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-140-8

Query Match 100.0%; Score 170; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
DB 298 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 327

## RESULT 8

US-08-485-938A-8  
Sequence 8, Application US/08485938A  
Patent No. 5847088  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,938A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 6-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5847088and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32792  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-938A-8

Query Match 100.0%; Score 170; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
DB 298 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 327

## RESULT 9

US-08-910-041-8  
Sequence 8, Application US/08910041  
Patent No. 5977308  
GENERAL INFORMATION:

APPLICANT: Cousins, Lawrence S.  
 APPLICANT: Eberhardt, Christine D.  
 APPLICANT: Gray, Patrick W.  
 APPLICANT: Le Trong, Hai  
 APPLICANT: Tjoelker, Larry W.  
 APPLICANT: Wilder, Cheryl L.  
 TITLE OF INVENTION: Platelet-Activating Factor  
 TITLE OF INVENTION: Acetylhydrolase  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,041  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/483,232  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/318,905  
 FILING DATE: 06-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/133,803  
 FILING DATE: 06-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rin-Laures, Li-Hsien  
 REGISTRATION NUMBER: 33,547  
 REFERENCE/DOCKET NUMBER: 27866/34026  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3658  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 441 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-910-041-8

Query Match 100.0%; Score 170; DB 2; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFYQYPAN 30  
 Db 298 WMFPLGDEVYSRIPQPLFFINSEYFYQYPAN 327

RESULT 10  
 US-09-328-474-8  
 ; Sequence 8, Application US/09328474  
 ; Patent No. 6045794  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cousins, Lawrence S.  
 ; APPLICANT: Eberhardt, Christine D.  
 ; APPLICANT: Gray, Patrick W.  
 ; APPLICANT: Le Trong, Hai  
 ; APPLICANT: Tjoelker, Larry W.  
 ; APPLICANT: Wilder, Cheryl L.  
 ; TITLE OF INVENTION: Platelet-Activating Factor  
 ; TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/328,474  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/483,232  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/318,905  
 FILING DATE: 06-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/133,803  
 FILING DATE: 06-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rin-Laures, Li-Hsien  
 REGISTRATION NUMBER: 33,547  
 REFERENCE/DOCKET NUMBER: 27866/34026  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3658  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 441 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-328-474-8

Query Match 100.0%; Score 170; DB 3; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFYQYPAN 30  
 Db 298 WMFPLGDEVYSRIPQPLFFINSEYFYQYPAN 327

RESULT 11  
 US-09-100-546-8  
 ; Sequence 8, Application US/09100546  
 ; Patent No. 6099836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cousins, Lawrence S.  
 ; APPLICANT: Eberhardt, Christine D.  
 ; APPLICANT: Gray, Patrick W.  
 ; APPLICANT: Le Trong, Hai  
 ; APPLICANT: Tjoelker, Larry W.  
 ; APPLICANT: Wilder, Cheryl L.  
 ; TITLE OF INVENTION: Platelet-Activating Factor  
 ; TITLE OF INVENTION: Acetylhydrolase  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,546  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
FILING DATE: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6099836and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-100-546-8

Query Match 100.0%; Score 170; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
|||||  
DB 298 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 327

RESULT 12  
US-09-010-715-8  
Sequence 8, Application US/09010715  
Patent No. 6146625  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6146625and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-010-715-8

Query Match 100.0%; Score 170; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 30  
|||||  
DB 298 WMFPLGDEVYSRIPQLFFINSEYFOYPAN 327

RESULT 13  
US-09-577-758-8  
Sequence 8, Application US/09577758  
Patent No. 6203790  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/577,758  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/010,715  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6203790and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0446  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-577-758-8

Query Match 100.0%; Score 170; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.4e-19;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
DB 298 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 327

## RESULT 14

US-08-485-938A-33

Sequence 33, Application US/08485938A

Patent No. 5847088

GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.

APPLICANT: Eberhardt, Christine D.

APPLICANT: Gray, Patrick W.

APPLICANT: Le Trong, Hai

APPLICANT: Tjoelker, Larry W.

APPLICANT: Wilder, Cheryl L.

TITLE OF INVENTION: Platelet-Activating Factor

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,938A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,905

FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,803

FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5847088and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/32792

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-938A-33

Query Match 91.2%; Score 155; DB 2; Length 444;  
Best Local Similarity 90.0%; Pred. No. 1.1e-16;  
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
DB 299 WMFPLGDEVYSRIPQPLFFINSEYFOYPSN 328

## RESULT 15

US-08-483-140-28

Sequence 28, Application US/08483140

Patent No. 5698403

GENERAL INFORMATION:

APPLICANT: ICOS Corporation

TITLE OF INVENTION: Platelet-Activating Factor Acetyl

TITLE OF INVENTION: Hydrolase

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,140

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,905

FILING DATE: 6-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,803

FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5698403and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32781

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-140-28

Query Match 77.6%; Score 132; DB 1; Length 444;  
Best Local Similarity 76.7%; Pred. No. 4.9e-13;  
Matches 23; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30  
DB 299 WMLPLDDAIYSRIPQPLFFINSEYFOYPSN 328

Search completed: March 9, 2002, 00:32:59  
Job time: 400 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:07 ; Search time 53.53 Seconds  
(without alignments)  
42,691 Million cell updates/sec

Title: US-09-922-067-2

Perfect score: 170  
Sequence: 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	170	100.0	441	2 S60247	platelet-activatin
2	128	75.3	436	2 JC5021	platelet-activatin
3	57	33.5	384	2 T32756	hypothetical prote
4	53	31.2	476	2 T28936	hypothetical prote
5	52	30.6	215	2 F71101	hypothetical prote
6	52	30.6	760	2 S64023	ALK1 protein - yea
7	52	30.6	1038	2 JC5027	115K outer membran
8	51	30.0	182	2 T61198	lipoxigenase (EC 1
9	51	30.0	313	2 T11153	NADH dehydrogenase
10	51	30.0	862	2 T05941	lipoxigenase (EC 1
11	50.5	29.7	835	2 S63463	hypothetical prote
12	50.5	29.7	920	2 A36887	endo-alpha-sialida
13	49.5	29.1	583	2 B82744	conserved hypothet
14	49.5	29.1	1658	2 T42642	phosphoinositide 3
15	49	28.8	399	2 S73452	protein trsb - Myc
16	49	28.8	399	2 S68805	pectin acetyl ester
17	49	28.8	489	2 C75269	hypothetical prote
18	49	28.8	600	2 E86854	hypothetical prote
19	49	28.8	735	2 D86465	probable integral
20	48.5	28.5	91	2 T17521	hypothetical prote
21	48.5	28.5	828	2 S34695	hypothetical prote
22	48	28.2	216	2 G85642	hypothetical prote
23	48	28.2	266	2 S73887	MD133 homolog A65
24	48	28.2	546	2 C56976	transfer complex p
25	48	28.2	690	2 T27357	hypothetical prote
26	48	28.2	726	2 T35865	probable cyclase -
27	47.5	27.9	1063	2 T38732	probable helicase
28	47.5	27.9	1155	2 E82144	transcription-repa
29	47	27.6	448	1 B42022	transcription fact

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Tjoecker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TIO>

A:Cross-references: EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g780133

Query Match

Best Local Similarity 100.0%; Score 170; DB 2; Length 441;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

Db 298 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 327

RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAP-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C:Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, J.

J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KARL>

A:Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAAL1054.1; PID:g1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 121-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: this enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>

F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.3%; Score 128; DB 2; Length 436;  
Best Local Similarity 80.8%; Pred. No. 6.2e-11;  
Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFQ 26  
||||:||||:||||:||||:||||:||||:  
Db 296 WMFPVGDVHSKIPQPLFFINSEYFQ 321

RESULT 3  
T32756  
hypothetical protein W03G9.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T32756  
R:Dante, M.; Keppler, D.  
A:Description: The sequence of C. elegans cosmid W03G9.  
A:Reference number: Z21220  
A:Accession: T32756  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-384 <DAN>  
A:Cross-references: EMBL:AF039716; PIDN:AAH96738.1; GSPDB:GN00019; CESP:W03G9.6  
A:Experimental source: strain Bristol N2; clone W03G9  
C:Genetics:  
A:Gene: CESP:W03G9.6  
A:Map position: 1  
A:Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 33.5%; Score 57; DB 2; Length 384;  
Best Local Similarity 33.3%; Pred. No. 1.3;  
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFQYFQY 30  
|||:||||:||||:||||:||||:||||:  
Db 259 WMYPLDQEQEAKQIPMLFNVGDWQWEN 288

RESULT 4  
T28936  
hypothetical protein C52B9.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T28936  
R:Nelson, J.  
A:Submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of C. elegans cosmid C52B9.  
A:Reference number: Z20545  
A:Accession: T28936  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-476 <NEL>  
A:Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN00028; CESP:C52B9.7  
A:Experimental source: strain Bristol N2; clone C52B9  
C:Genetics:  
A:Gene: CESP:C52B9.7  
A:Map position: X  
A:Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 31.2%; Score 53; DB 2; Length 476;  
Best Local Similarity 33.3%; Pred. No. 6.3;  
Matches 10; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFQYFQY 30  
||:||||:||||:||||:||||:||||:  
Db 351 WMYPLDSTQEQAKQPTLFNVGDWQWEN 380

RESULT 5

Query Match 30.6%; Score 52; DB 2; Length 760;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 4 PLGDEVYSRIPQPLFFINSE 23  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 636 PQDDVLVLRDHPFLFLNGK 655

RESULT 7  
JC6027  
I15K outer membrane protein precursor - Bacteroides thetaiotaomicron  
N:Alternate names: SusC protein  
C:Species: Bacteroides thetaiotaomicron

Query Match 30.6%; Score 52; DB 2; Length 760;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 4 PLGDEVYSRIPQPLFFINSE 23  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 636 PQDDVLVLRDHPFLFLNGK 655

RESULT 7  
JC6027  
I15K outer membrane protein precursor - Bacteroides thetaiotaomicron  
N:Alternate names: SusC protein  
C:Species: Bacteroides thetaiotaomicron

F71101  
hypothetical protein PH1073 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 18-Aug-2000  
C:Accession: F71101  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.;  
M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, T.; Yamazaki, J.; Kushida, N.;  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137  
A:Accession: F71101  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-215 <KAW>  
A:Cross-references: CB:AP000004; NID:g3236131; PIDN:BAA30172.1; PID:d1031115; PID:  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by Ge  
C:Genetics:  
A:Gene: PH1073  
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1073

Query Match 30.6%; Score 52; DB 2; Length 215;  
Best Local Similarity 42.9%; Pred. No. 3.5;  
Matches 12; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 MFPLGDEVYSRIPQPLFFINSEYFQYPA 29  
:||||:||||:||||:||||:||||:  
Db 123 VFPLTIISMYSSIVTVLFSSRSRLAWPS 150

RESULT 6  
S64023  
ALK1 protein - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein G3686; protein YGL021w  
C:Species: Saccharomyces cerevisiae  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 29-Oct-1999  
C:Accession: S64023; S57396  
R:Hebling, U.; Hofmann, B.; Delius, H.  
A:Submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64003  
A:Accession: S64023  
A:Molecule type: DNA  
A:Residues: 1-760 <HEB>  
A:Cross-references: EMBL:272543; NID:gl322486; PIDN:CAA96721.1; PID:e243850; PID:g  
A:Experimental source: strain S288C  
R:Rognes, T.  
A:Submitted to the EMBL Data Library, May 1995  
A:Reference number: S57396  
A:Accession: S57396  
A:Molecule type: DNA  
A:Residues: 1-757, 'AL' <ROG>  
A:Cross-references: EMBL:X87672; NID:g861109; PIDN:CAA61012.1; PID:g861110  
C:Genetics:  
A:Gene: SGD:ALK1  
A:Cross-references: SGD:S0002989; MIPS:YGL021w  
A:Map position: 7L

Query Match 30.6%; Score 52; DB 2; Length 760;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 4 PLGDEVYSRIPQPLFFINSE 23  
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 636 PQDDVLVLRDHPFLFLNGK 655

RESULT 7  
JC6027  
I15K outer membrane protein precursor - Bacteroides thetaiotaomicron  
N:Alternate names: SusC protein  
C:Species: Bacteroides thetaiotaomicron



C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 08-Oct-1999  
C:Accession: JCG6027

R:Reeves, A.R.; D'Elia, J.N.; Frias, J.; Salyers, A.A.

J. Bacteriol. 178, 823-830, 1996

A:Title: A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of acetate

A:Reference number: JCG6027; MUID:96146534

A:Accession: JCG6027

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-1038 <REE>

A:Cross-references: GB:L49338; NID:g1100064; PIDN:AAA95938.1; PID:g1100065

A:Note: It is uncertain whether Met-14 or Met-20 is the initiator

C:Comment: This protein is an integral outer membrane protein, and it is essential for utilization of acetate

C:Genetics:

A:Gene: susC

C:Keywords: transmembrane protein

F:1-39/Domain: signal sequence #status predicted <SIG>

F:40-1038/Product: 115K outer membrane protein #status predicted <MAT>

F:1028-1038/Domain: transmembrane #status predicted <TM>

Query Match 30.6%; Score 52; DB 2; Length 1038;

Best Local Similarity 61.5%; Pred. No. 22;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 PLFFINSEYFQYP 28

||| : ||| |||

Db 664 PLYVWVNEAQP 676

RESULT 8

T06198

lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000

R:Rouster, J.; Leah, R.; Mundy, J.; Cameron-Mills, V.

Plant J. 11, 513-523, 1997

A:Title: Identification of a methyl jasmonate-responsive region in the promoter of a lipid transfer protein

A:Reference number: Z15527; MUID:97260963

A:Accession: T06198

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-182 <NOU>

A:Cross-references: EMBL:U83904; NID:g1814015; PIDN:AAB41791.1; PID:g1814016

C:Genetics:

A:Gene: Lox1

A:Introns: 65/1; 163/3

C:Superfamily: lipoxigenase

C:Keywords: oxidoreductase

Query Match 30.0%; Score 51; DB 2; Length 182;

Best Local Similarity 38.7%; Pred. No. 4;

Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYF--QYPA 29

||| : ||| : ||| : |||

Db 146 WIYPAANYRSRV----FFANDTLPQMPA 172

RESULT 9

T11153

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - hardbacked tick (Rhizoglyphus

C:Species: mitochondrion Rhizoglyphus sanguineus

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 05-May-2000

C:Accession: T11153

R:Black IV, W.C.; Roehrdanz, R.L.

Mol. Biol. Evol. 15, 1772-1785, 1998

A:Title: Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate

A:Reference number: Z17252; MUID:99083443

A:Accession: T11153

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <BLA>

A:Cross-references: EMBL:AF081829; NID:g4164556; PID:g4164557; PIDN:AA005517.1

C:Genetics:

A:Genome: mitochondrion

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 30.0%; Score 51; DB 2; Length 313;

Best Local Similarity 66.7%; Pred. No. 7.6;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 YSRIPQPLFFINSEY 24

||| ||| ||| ||| |||

Db 270 YLRILTLPFFINSKF 284

RESULT 10

T05941

lipoxigenase (EC 1.13.11.12) 1 - barley

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000

C:Accession: T05941

R:van Mechelen, J.R.; Smits, M.; Douma, A.C.; Rouster, J.; Cameron-Mills, V.; Heidekamp

Biochim. Biophys. Acta 1254, 221-225, 1995

A:Title: Primary structure of a lipoxigenase from barley grain as deduced from its cDNA

A:Reference number: Z15463; MUID:95127754

A:Accession: T05941

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-862 <VAN>

A:Cross-references: EMBL:L35931; NID:g532571; PIDN:AAA64893.1; PID:g532572

C:Genetics:

A:Gene: LoxA

C:Superfamily: lipoxigenase

C:Keywords: oxidoreductase

Query Match 30.0%; Score 51; DB 2; Length 862;

Best Local Similarity 38.7%; Pred. No. 25;

Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYF--QYPA 29

||| : ||| : ||| : |||

Db 146 WIYPAANYRSRV----FFANDTLPQMPA 172

RESULT 11

S63463

hypothetical protein YPL019c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein LPB12c

C:Species: Saccharomyces cerevisiae

C>Date: 16-May-1996 #sequence\_revision 12-Jul-1996 #text\_change 05-Nov-1999

C:Accession: S63463

R:Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.

submitted to the EMBL Data Library, September 1995

A:Reference number: S63462

A:Accession: S63463

A:Molecule type: DNA

A:Residues: 1-835 <WAN>

A:Cross-references: EMBL:U36624; NID:g1276642; PID:g1039458; GSPDB:GN00016; MIPS:YPL019c

C:Genetics:

A:Gene: MIPS:YPL019c

A:Map position: 16L

Query Match 29.7%; Score 50.5; DB 2; Length 835;

Best Local Similarity 43.5%; Pred. No. 28;

Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 7 DEVYSRIPOPLFFINS-EYFQYP 28

||| : ||| ||| : |||

Db 466 DDIDSINPNPLRAGEYSKFP 488

RESULT 12  
A36887  
endo-alpha-sialidase (EC 3.2.1.129), tail - phage K1F  
N:Alternate names: endo-N-acylneuraminidase  
C:Species: phage K1F  
C>Date: 18-Nov-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A36887  
R:Pattar, J.G.; Vimr, E.R.  
J. Bacteriol. 175, 4354-4363, 1993  
A:Title: Complete nucleotide sequence of the bacteriophage K1F tail gene encoding endo-N-  
A:Reference number: A36887; MUID:93322313  
A:Accession: A36887  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-920 <P>  
A:Cross-references: GB:M63657; NID:q215082; PIDN:AAC37340.1; PID:q215083  
A:Note: in the authors' translation residues 875-888 are shown after residue 903 and, co  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation; tail protein

Query Match 29.7%; Score 50.5; DB 2; Length 920;  
Best Local Similarity 52.6%; Pred. No. 32;  
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 9 VYRIP-QLFFINSEYFQ 26  
||| ||| ||| : : : : :  
Db 295 VYRIPQPLYYASEEPVQ 313

RESULT 13  
B82744  
conserved hypothetical protein XF0929 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: B82744  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: B82744  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-583 <SIM>  
A:Cross-references: GB:AE003932; GB:AE003849; NID:99105849; PIDN:AAF83739.1; GSPDB:GN001  
R:Simpson, A.J.G.; Reinach, F.C.; Abruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorcy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak  
M.; Tshuko, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.; Z

Query Match 29.1%; Score 49.5; DB 2; Length 583;  
Best Local Similarity 34.6%; Pred. No. 26;  
Matches 9; Conservative 8; Mismatches 8; Indels 1; Gaps 1;  
QY 1 WMPF-LGDEVYSRIPQPLFFINSEYF 25  
||| ||| ||| : : : : :  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF0929

Db 53 WLFPHRGNELYSDKPPMLMWLQAAFY 88

RESULT 14  
T42642  
phosphoinositide 3-kinase (EC 2.7.1.1) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-May-2000  
C:Accession: T42642  
R:Moiz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.  
J. Biol. Chem. 271, 13892-13899, 1996  
A:Title: Cpk is a novel class of Drosophila ptdIns 3-kinase containing a C2 domain  
A:Reference number: 217659; MUID:96278830  
A:Accession: T42642  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1658 <M>  
A:Cross-references: EMBL:U52193; NID:g1272421; PID:g1272422; PIDN:AAC52604.1  
A:Experimental source: strain balb c  
C:Genetics:  
A:Gene: cpk  
C:Superfamily: HSC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homo  
C:Keywords: phosphotransferase

Query Match 29.1%; Score 49.5; DB 2; Length 1658;  
Best Local Similarity 42.3%; Pred. No. 88;  
Matches 11; Conservative 2; Mismatches 8; Indels 5; Gaps 1;

QY 3 PPLGDEVYSRIPQPLFFINSEYFQYP 28  
||| ||| ||| : : : : :  
Db 179 FPSTESVVLRLPG-----QSPYFSYP 199

RESULT 15  
S73452  
protein trsb - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein B01\_orf299V  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C>Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73452  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneu  
A:Reference number: S73327; MUID:97105885  
A:Accession: S73452  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-299 <HIM>  
A:Cross-references: EMBL:AE000015; GB:U00089; NID:g1673779; PIDN:AAB95774.1; PID:gi1673779  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: trsb  
A:Genetic code: SGC3  
A:Start codon: GTG  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 28.8%; Score 49; DB 2; Length 299;  
Best Local Similarity 34.5%; Pred. No. 14;  
Matches 10; Conservative 5; Mismatches 6; Indels 8; Gaps 1;

QY 10 YSRIPQPLFFI-----NSEYFQYPAN 30  
||| ||| ||| : : : : :  
Db 271 YTWLQPLAFIFGGLMALTRKYIRPKN 299

Search completed: March 9, 2002, 00:34:10  
Job time: 321 sec





GenCore version 4.5

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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:33 ; Search time 30.16 seconds

(without alignments)

36.470 Million cell updates/sec

Title: us-09-922-067-2

Perfect score: 170

Sequence: 1 WMFPLGDEVYRIPQPLFFINSEVFQYPAN 30

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	100.0	441	1 PAPA_HUMAN	Q13093 h platelet-
2	155	91.2	444	1 PAPA_BOVIN	Q28017 b platelet-
3	132	77.6	444	1 PAPA_CANFA	Q28262 c platelet-
4	128	75.3	436	1 PAPA_CAVPO	P70683 c platelet-
5	100.5	59.1	422	1 PAPA_CHICK	Q30678 g platelet-
6	96	56.5	440	1 PAPA_MOUSE	Q50963 m platelet-
7	78	45.9	392	1 PAF2_HUMAN	Q99487 homo sapien
8	77	45.3	392	1 PAF2_BOVIN	P79106 bos taurus
9	53	31.2	476	1 PAF2_HUMAN	Q22943 caenorhabdi
10	52.5	30.9	483	1 MM20_HUMAN	Q60882 homo sapien
11	52	30.6	760	1 ALK1_YEAST	P43633 saccharomyc
12	51	30.0	313	1 NUX2M_RHISA	Q99817 rhipicephal
13	51	30.0	862	1 LOX1_HORVU	P29114 horddeum vul
14	50.5	29.7	919	1 ENAN_BK1F	Q04830 bacterioph
15	49.5	29.1	482	1 MM20_MOUSE	P37748 mus musculu
16	49	28.8	299	1 Y025_MYCPN	P75086 mycoplasma
17	48.5	28.5	828	1 YKR6_YEAST	P34239 saccharomyc
18	48	28.2	266	1 Y133_MYCPN	P75503 mycoplasma
19	47	27.6	692	1 VP3_ROTTC	P26192 porcine rot
20	47	27.6	754	1 SULX_YEAST	P53394 saccharomyc
21	47	27.6	1155	1 ROM1_YEAST	P53046 saccharomyc
22	46	27.1	804	1 SCV1_YEAST	P53009 saccharomyc
23	45.5	26.8	399	1 FTSM_BUCAL	P57312 buchmera ap
24	45.5	26.8	607	1 HEMA_CDVC	O65999 canine dist
25	45.5	26.8	941	1 SYL_HAEIN	P43824 haemophilus
26	45	26.5	152	1 VGD_BPG4	P03638 bacterioph
27	45	26.5	317	1 SPD2_DATST	Q96557 datura stra
28	45	26.5	342	1 SPDE_LYCES	O92s45 lycopersico
29	44.5	26.2	709	1 SVT_ARATH	O04630 arabidopsis
30	44	25.9	181	1 FLAV_RHOCA	P52967 rhodobacter
31	44	25.9	210	1 SOMA_CYPCA	P10298 cyprinus ca
32	44	25.9	297	1 YPHB_BACSU	P50742 bacillus su
33	44	25.9	299	1 YFAD_ECOLI	P37014 escherichia

Q10325 schizosacch  
Q58867 methanococc  
P38250 saccharomyc  
P40879 homo sapien  
Q09550 caenorhabdi  
Q15404 homo sapien  
Q01730 mus musculu  
Q9pjf9 chlamydia m  
P12332 bradyrhizob  
P55359 rhizobium s  
Q50336 mycoplasma  
P21339 saccharomyc

## ALIGNMENTS

RESULT 1

PAPA\_HUMAN

STANDARD;

PRT: 441 AA.

AC Q13093; Q15692;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
GN PLA2G7 OR PAFAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.  
RC TISSUE=Myeloid;  
RX MEDLINE=95214779; PubMed=7700381;  
RA Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,  
RA Schimpf B., Hooper S., le Trong H., Couzens L.S., Zimmerman G.A.,  
RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;  
RA "Anti-inflammatory properties of a platelet-activating factor  
acetylhydrolase.";  
RL Nature 374:549-553(1995).  
RP [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Lymphoma;  
RX MEDLINE=96197208; PubMed=8624782;  
RA Tew D.G., Southan C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,  
RA Moores K., Gloger I.S., Macphie C.H.;  
RA "Purification, properties, sequencing, and cloning of a lipoprotein-  
associated, serine-dependent phospholipase involved in the oxidative  
modification of low-density lipoproteins.";  
RL Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).  
RP [3]  
RP MUTAGENESIS.  
RX MEDLINE=96029630; PubMed=7592717;  
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
RA Gray P.W.;  
RA "Plasma platelet-activating factor acetylhydrolase is a secreted  
phospholipase A2 with a catalytic triad.";  
RL J. Biol. Chem. 270:25481-25487(1995).  
RN [4]  
RP VARIANT PHE-279.  
RX MEDLINE=96259525; PubMed=8675689;  
RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,  
RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,  
RA McIntyre T.M., Gray P.W., Prescott S.M.;  
RA "Platelet-activating factor acetylhydrolase deficiency. A missense  
mutation near the active site of an anti-inflammatory  
phospholipase.";  
RL J. Clin. Invest. 97:2784-2791(1996).  
RN [5]



PAFA\_CANFA  
ID PAFA\_CANFA STANDARD; PRT; 444 AA.  
AC Q28262;  
DT 01-NOV-1997 (Rel. 35, Created)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
GN PLA2G7.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96029630; PubMed=7592717;  
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
RT phospholipase A2 with a catalytic triad.";  
RL J. Biol. Chem. 270:25481-25487(1995).  
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC PHOSPHOLIPIDS.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: PLASMA.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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CC  
CC EMBL: U34246; AAC48484.1; -  
CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
CC DR PROSITE: PS00120; LIPASE\_SER; 1.  
CC DR Hydrolase; Lipid degradation; Glycoprotein; Signal.  
CC KW SIGNAL 1 21 BY SIMILARITY  
CC FT CHAIN 22 444 PLATELET-ACTIVATING FACTOR  
CC FT ACT\_SITE 274 274 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 297 297 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 444 AA; 50136 MW; 814F0AE3B074AC CRC64;  
Query Match 77.6%; Score 132; DB 1; Length 444;  
Best Local Similarity 76.7%; Pred. No. 1.9e-11;  
Matches 23; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 WMPPLGDEVYSRIPOPLFFINSEYFOYPAN 30  
DB 299 WMLPLDDAIYSRIQPPLFFINSEYFOFFEN 328  
RESULT 4  
PAFA\_CANFO  
ID PAFA\_CANFO STANDARD; PRT; 436 AA.

P70683;  
AC 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
GN PLA2G7 OR PAFAH.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=HARTLEY; TISSUE=Liver;  
RX MEDLINE=97103479; PubMed=8947850;  
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,  
RA Yokoyama K., Setaka M., Nojima S.;  
RT "Cloning, expression and characterization of plasma  
RT platelet-activating factor-acetylhydrolase from guinea pig.";  
RL J. Biochem. 120:838-844(1996).  
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC PHOSPHOLIPIDS.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: PLASMA.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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CC  
CC EMBL: D67037; BAA11054.1; -  
CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
CC DR PROSITE: PS00120; LIPASE\_SER; 1.  
CC DR Hydrolase; Lipid degradation; Glycoprotein; Signal.  
CC KW SIGNAL 1 21 BY SIMILARITY  
CC FT CHAIN 22 436 PLATELET-ACTIVATING FACTOR  
CC FT ACT\_SITE 271 271 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 436 AA; 49062 MW; C359D96E392FFE11 CRC64;  
Query Match 75.3%; Score 128; DB 1; Length 436;  
Best Local Similarity 80.8%; Pred. No. 7.1e-11;  
Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WMPPLGDEVYSRIPOPLFFINSEYFQ 26  
DB 296 WMPFVGEDVHSKIPQLFFINSEYFQ 321  
RESULT 5  
PAFA\_CHICK  
ID PAFA\_CHICK STANDARD; PRT; 422 AA.  
AC Q90678;  
DT 01-NOV-1997 (Rel. 35, Created)





DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).  
 GN PAFAH2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC MEDLINE=97115847; PubMed=8955149;  
 RX Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
 RA Aoki J., Hattori M., Arai H., Inoue K.;  
 RT "cDNA cloning and expression of intracellular platelet-activating  
 factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
 acetylhydrolase.";  
 RL J. Biol. Chem. 271:33032-33038(1996).  
 RN [2]  
 RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.  
 RP TISSUE=Prostate;  
 RC MEDLINE=98161812; PubMed=9494101;  
 RX Rice S.Q.J., Southern C., Boyd H.F., Terrett J.A., Macphie C.H.,  
 RA Moores K., Glover I.S., Tew D.G.;  
 RT "Expression, purification and characterization of a human  
 serine-dependent phospholipase A2 with high specificity for oxidized  
 phospholipids and platelet activating factor.";  
 RL Biochem. J. 330:1309-1315(1998).  
 RN [3]  
 RN REVIEW.  
 RP MEDLINE=97364701; PubMed=9218411;  
 RX Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
 RA "Platelet-activating factor acetylhydrolases.";  
 RL J. Biol. Chem. 272:17895-17898(1997).  
 CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
 ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
 FUNCTION WITH THE PLASMA-TYPE ENZYME.  
 CC -2- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -3- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,  
 3,4-DICHLOROISOCOUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DIPP) AND  
 DIETHYL P-NITROPHENYL PHOSPHATE (DENP).  
 CC -4- SUBUNIT: MONOMER.  
 CC -5- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -6- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT  
 HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO  
 AMYGDALA AND FRONTAL CORTEX.  
 CC -7- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.  
 CC -8- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
 CC  
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 CC  
 CC EMBL: D87845; BAA13468.1; -;  
 CC EMBL: U89386; AAC39707.1; -;  
 CC MIM: 602344;  
 CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 CC InterPro: IPR000734; Lipase.  
 CC PROSITE: PS00120; LIPASE\_SER; 1.  
 CC Hydrolase; Lipid degradation.  
 KW ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CONFLICT 212 212 L -> F (IN REF. 2).  
 SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;

Query Match 45.9%; Score 78; DB 1; Length 392;  
 Best Local Similarity 53.8%; Pred. No. 0.00085;  
 Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFQ 26  
 I I I I I : : : : I I I I I : :  
 DB 261 WMFPLRDFYPKARGPVFFINTEKFKQ 286

RESULT 8  
 PAF2\_BOVIN  
 ID PAF2\_BOVIN STANDARD; PRT; 392 AA.  
 AC P79106;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC  
 DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).  
 GN PAFAH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP TISSUE=Kidney;  
 RC MEDLINE=97115847; PubMed=8955149;  
 RX Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
 RA Aoki J., Hattori M., Arai H., Inoue K.;  
 RT "cDNA cloning and expression of intracellular platelet-activating  
 factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
 acetylhydrolase.";  
 RL J. Biol. Chem. 271:33032-33038(1996).  
 RN [2]  
 RN REVIEW.  
 RP MEDLINE=97364701; PubMed=9218411;  
 RX Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
 RA "Platelet-activating factor acetylhydrolases.";  
 RL J. Biol. Chem. 272:17895-17898(1997).  
 CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
 ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
 FUNCTION WITH THE PLASMA-TYPE ENZYME.  
 CC -2- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -3- SUBUNIT: MONOMER.  
 CC -4- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -5- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT  
 LOWER LEVELS IN OTHER TISSUES.  
 CC -6- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D87559; BAA13419.1; -;  
 CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 CC InterPro: IPR000734; Lipase.  
 CC PROSITE: PS00120; LIPASE\_SER; 1.  
 CC Hydrolase; Lipid degradation.  
 KW ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 SQ SEQUENCE 392 AA; 43865 MW; 1DEAC2ADFA6CEA8 CRC64;

Query Match 45.3%; Score 77; DB 1; Length 392;  
 Best Local Similarity 53.8%; Pred. No. 0.0012; 9; Indels 0; Gaps 0;  
 Matches 14; Conservative 3; Mismatches 9;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFQ 26  
 I I I I I : : : : I I I I I : :  
 DB 261 WMFPLRDFYPKARGPVFFINTEKFKQ 286



```

QY 9 VYSRIPO-PLFINSFSEYFOY 27
DB 398 VYLREPQTLFFVGVDEYIS 417

RESULT 11
ID ALK1_YEAST STANDARD; PRT; 760 AA.
AC P43633;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE DNA DAMAGE-RESPONSE PROTEIN ALK1.
GN ALK1 OR YGL021W OR G3686.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rognes F.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YBL009W.
-----
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-----
DR EMBL; X87672; CAA61012.1; -
DR EMBL; 272543; CAA96721.1; -
DR SGD; S0002989; ALK1.
KW DNA damage.
FT DOMAIN 240 245 POLY-GLN.
FT DOMAIN 264 269 POLY-SER.
FT DOMAIN 351 356 POLY-SER.
FT CONFLICT 758 760 LYK -> AL (IN REF. 1).
SQ SEQUENCE 760 AA; 86086 MW; 3FD169AD789ED60A CRC64;

Query Match 30.6%; Score 52; DB 1; Length 760;
Best Local Similarity 45.0%; Pred. NO. 8.6;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 PLGDEVYSRIPOPLFFINSF 23
DB 636 PQDDVLYRLDHPFLFLNGK 655

RESULT 12
ID NU2M_RHISA STANDARD; PRT; 313 AA.
AC O99817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
GN NU2.
OS Rhinipcephalus sanguineus (Brown dog tick).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhinipcephalus.
OX NCBI_TaxID=34632;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE-99083443; PubMed-9866211;
RA Black W.C. IV, Roehrdanz R.L.;
RT "Mitochondrial gene order is not conserved in arthropods: prostrate
RT and metastriate tick mitochondrial genomes.";
RL Mol. Biol. Evol. 15:1772-1785(1998).
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
-----
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-----
DR EMBL; AF081829; AAD05517.1; -
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 313 AA; 37059 MW; E6382AEDAF32B0B6 CRC64;

Query Match 30.0%; Score 51; DB 1; Length 313;
Best Local Similarity 66.7%; Pred. NO. 4.8;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 YSRIPOLPFFINSF 24
DB 270 YLRILTLPFFINSKF 284

RESULT 13
ID LOXL_HORVU STANDARD; PRT; 862 AA.
AC P29114; Q42845;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LIPOXYGENASE 1 (EC 1.13.11.12).
GN LOXL1 OR LOXA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV TRIUMPH;
RX MEDLINE-95127754; PubMed-7827128;
RA van Mechelen J.R., Smits M., Douma A.C., Rouster J., Cameron-Mills V.,
RA Heidekamp F., Valk B.E.;
RT "Primary structure of a lipoxygenase from barley grain as deduced
RT from its cDNA sequence.";
RL Biochim. Biophys. Acta 1254:221-225(1995).
RN [2]
RP SEQUENCE OF 274-294 AND 832-845.
RC STRAIN-CV TRIUMPH; TISSUE-Embryo;
RX MEDLINE-92207997; PubMed-1554746;
RA Doderer A., Kokkelink I., van der Veen S., Valk B.E., Schram A.W.,
RA Douma A.C.;
RT "Purification and characterization of two lipoxygenase isoenzymes
RT from germinating barley.";
RL Biochim. Biophys. Acta 1120:97-104(1992).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
CC WOUNDING.
CC -!- CATALYTIC ACTIVITY: HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS,
CC CIS-1,4-PENTADIENE STRUCTURE.
CC -!- COFACTOR: IRON, ONE ATOM TIGHTLY BOUND PER MOLECULE.

```

CC -!- SUBUNIT: MONOMER.  
CC -!- MISCELLANEOUS: WITH LINOLEATE AS SUBSTRATE, LIPOXYGENASE 1 SHOWS A  
CC SPECIFICITY FOR CARBON 9 AS THE SITE FOR HYDROPEROXIDATION (IN  
CC CONTRAST TO LIPOXYGENASE 2, WHICH SHOWS A PREFERENCE FOR CARBON  
CC 13).  
CC -!- SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: L35931; AAA64893.1; -  
CC HSSP: P08170; 2SBL.  
CC InterPro: IPR001024; LH2.  
CC InterPro: IPR000907; Lipoxigenase.  
CC Pfam: PF00305; lipoxigenase; 1.  
CC Pfam: PF01477; PLAT; 1.  
CC PRINTS: PR00087; LIPOXYGENASE.  
CC PRINTS: PR00468; ELTLPOXGNASE.  
CC SMART: SM00308; LH2; 1.  
CC PROSITE: PS00711; LIPOXYGENASE\_1; 1.  
CC PROSITE: PS00081; LIPOXYGENASE\_2; FALSE\_NEG.  
CC Oxidoreductase; Dioxygenase; Iron; Multigene family.  
CC METAL 517 517  
CC METAL 522 522 IRON (BY SIMILARITY).  
CC METAL 708 708 IRON (BY SIMILARITY).  
CC METAL 862 862 IRON (BY SIMILARITY).  
CC METAL 862 862 IRON (BY SIMILARITY).  
CC SEQUENCE 862 AA; 96393 MW; F55954473467BEAA CRC64;  
CC  
CC Query Match 30.0%; Score 51; DB 1; Length 862;  
CC Best Local Similarity 38.7%; Pred. No. 14;  
CC Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;  
CC  
CC QY 1 WMFPLGDEVYSRTPQPLFFINSEVF--QYPA 29  
CC I::: :|||: |||: |||: |||  
CC Db 146 WYPAARYSRV-----FFANDYLPQMPA 172  
CC  
CC RESULT 14  
CC ENAN\_BPKIF STANDARD; PRT; 919 AA.  
CC ID ENAN\_BPKIF  
CC AC Q04830;  
CC DT 01-FEB-1995 (Rel. 31, Created)  
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)  
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)  
CC DE ENDO-N-ACETYLNEURAMINIDASE (EC 3.2.1.129) (ENDO-N) (ENDOSTALIDASE)  
CC DE (GI02).  
CC OS Bacteriophage KIF.  
CC OC Viruses.  
CC NCBI\_TaxID=12391;  
CC RN  
CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-30 AND 916-919.  
CC RX MEDLINE=93322313; PubMed=8331067;  
CC RA Pether J.G., Vlmr E.R.;  
CC RT "Complete nucleotide sequence of the bacteriophage KIF tail gene  
CC encoding endo-N-acylneuraminidase (endo-N) and comparison to an  
CC endo-N homolog in bacteriophage PK1E.";  
CC RL J. Bacteriol. 175:4354-4363(1993).  
CC CC -!- FUNCTION: RESPONSIBLE FOR INITIAL ABSORPTION OF THE PHAGE TO THE  
CC HOST BACTERIUM. DEGRADATION OF THE ALPHA-2,8-LINKED POLYSIALIC  
CC ACID K1 CAPSULE.  
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF ALPHA-2,8-SIALOSYL LINKAGES  
CC IN OLIGO OR POLY(SIALIC) ACIDS.  
CC -!- SUBUNIT: HOMOTRIMER.  
CC -!- SIMILARITY: BELONGS TO FAMILY 58 OF GLYCOSYL HYDROLASES.  
CC -!- SIMILARITY: CONTAINS 2 BNR REPEATS.  
CC

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CC  
CC EMBL: M63657; AAC37340.1; -  
CC InterPro: IPR002860; BNR.  
CC InterPro: IPR001724; Glyco\_hydro\_58.  
CC Pfam: PF02012; BNR; 2.  
CC PRINTS: PR00849; GLHYDRLASE58.  
CC Hydrolase; Glycosidase; Repeat.  
CC INIT\_MET 0  
CC FT DOMAIN 197 215 GLY-RICH (HINGE).  
CC FT SEQUENCE 919 AA; 101882 MW; DD35767126A4B68A CRC64;  
CC  
CC Query Match 29.7%; Score 50.5; DB 1; Length 919;  
CC Best Local Similarity 52.6%; Pred. No. 17;  
CC Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
CC  
CC QY 9 VYSRIP-QPLFFINSEYFQ 26  
CC ||||| |||: :|: |  
CC Db 294 VYKIPQPLYYASEEFVQ 312  
CC  
CC RESULT 15  
CC MM20\_MOUSE STANDARD; PRT; 482 AA.  
CC ID MM20\_MOUSE  
CC AC P57748;  
CC DT 20-AUG-2001 (Rel. 40, Created)  
CC DT 20-AUG-2001 (Rel. 40, Last sequence update)  
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)  
CC DE MATRIX METALLOPROTEINASE-20 PRECURSOR (EC 3.4.24.-) (MMP-20) (ENAMEL  
CC METALLOPROTEINASE) (ENAMELYSIN).  
CC GN MMP20.  
CC OS Mus musculus (Mouse).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CC OX NCBI\_TaxID=10090;  
CC [1]  
CC RN  
CC RP SEQUENCE FROM N.A.  
CC RC STRAIN=129/SVJ;  
CC RX MEDLINE=20079167; PubMed=10610728;  
CC RA Caterina J., Shi J., Krakora S., Bartlett J.D., Engler J.A.,  
CC Kozak C.A., Birkedal-Hansen H.;  
CC RT "Isolation, characterization, and chromosomal location of the mouse  
CC enamelysin gene.";  
CC RL Genomics 62:308-311(1999).  
CC CC -!- FUNCTION: DEGRADATES AMELOGENIN, THE MAJOR PROTEIN COMPONENT OF THE  
CC ENAMEL MATRIX AND TWO OF THE MACROMOLECULES CHARACTERISING THE  
CC CARTILAGE EXTRACELLULAR MATRIX: AGGREGAN AND THE CARTILAGE  
CC OLIGOMERIC MATRIX PROTEIN (COMP). MAY PLAY A CENTRAL ROLE IN TOOTH  
CC ENAMEL FORMATION (BY SIMILARITY).  
CC CC -!- CATALYTIC ACTIVITY: CLEAVES AGGREGAN AT THE 360-ASN-1-PHE-361 SITE  
CC (BY SIMILARITY).  
CC CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY (BY SIMILARITY).  
CC CC -!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR  
CC MATRIX (BY SIMILARITY).  
CC CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE ENAMEL ORGAN.  
CC CC -!- PTM: AUTOACTIVATES AT LEAST AT THE 106-ASN-1-TYR-107 SITE (BY  
CC SIMILARITY).  
CC CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.  
CC CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC  
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.  
CC  
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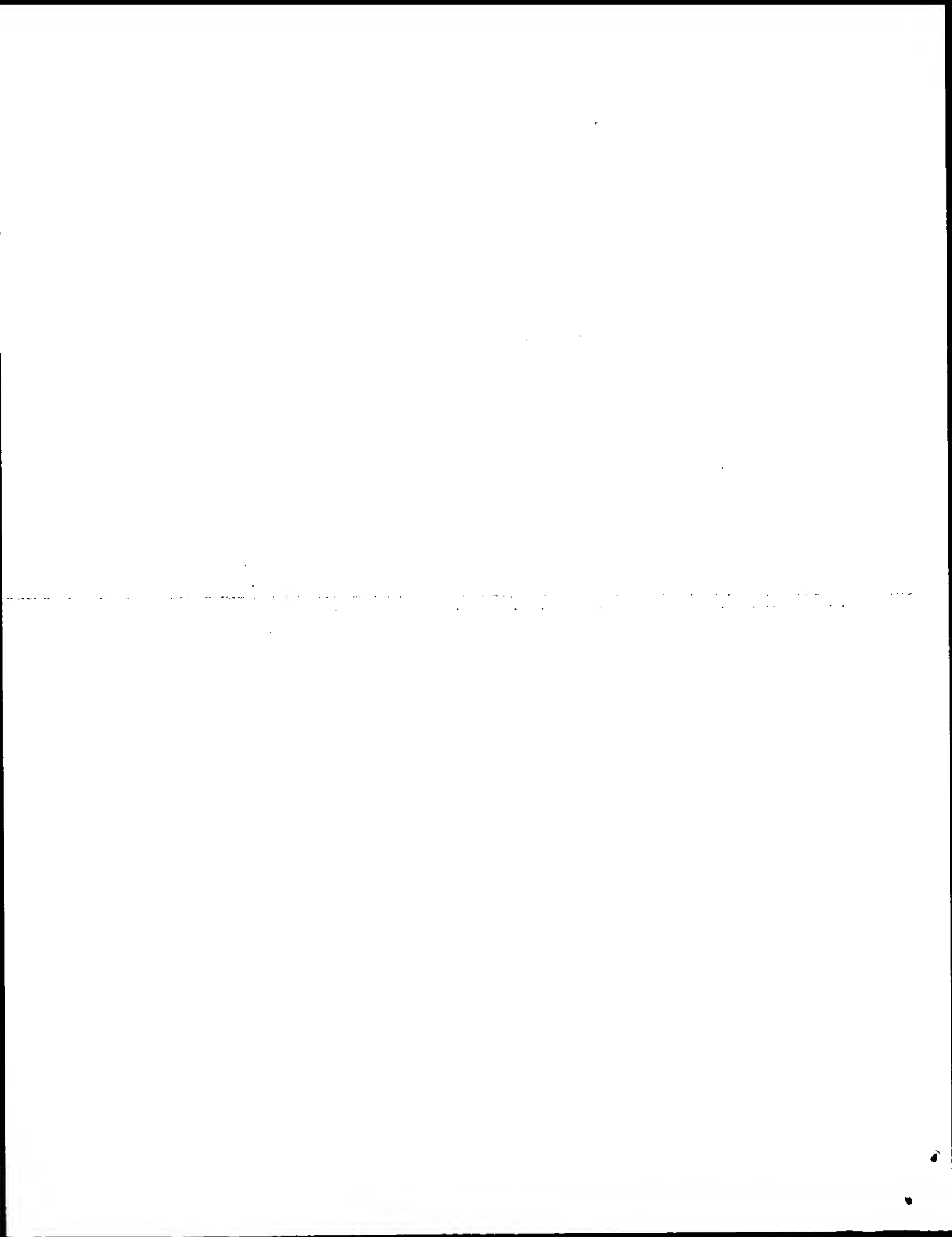
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 DR EMBL; AF156956; AAF28472.1; -  
 DR EMBL; AF156947; AAF28472.1; JOINED.  
 DR EMBL; AF156948; AAF28472.1; JOINED.  
 DR EMBL; AF156949; AAF28472.1; JOINED.  
 DR EMBL; AF156950; AAF28472.1; JOINED.  
 DR EMBL; AF156951; AAF28472.1; JOINED.  
 DR EMBL; AF156952; AAF28472.1; JOINED.  
 DR EMBL; AF156953; AAF28472.1; JOINED.  
 DR EMBL; AF156954; AAF28472.1; JOINED.  
 DR EMBL; AF156955; AAF28472.1; JOINED.  
 DR EMBL; AF155933; AAF28470.1; -  
 DR MEROPS; M10.019; -  
 DR MGD; MGI:1353466; Mmp20.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR003016; Lipovl.  
 DR InterPro; IPR001818; Matrixin.  
 DR InterPro; IPR000130; Zn\_MTpeptdse.  
 DR Pfam; PF00045; hemopexin; 4  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR SMART; SM00120; Hx; 4.  
 DR SMART; SM00235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; FALSE\_NEG.  
 KW Hydrolase; Metalloprotease; Zinc; Calcium; Zymogen; Signal;  
 KW Extracellular matrix.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT PROPEP 22 106 BY SIMILARITY.  
 FT CHAIN 107 482 MATRIX METALLOPROTEINASE-20.  
 FT DOMAIN 292 482 HEMOPEXIN-LIKE.  
 FT SITE 99 99 CYSTEINE SWITCH (POTENTIAL).  
 FT METAL 225 225 ZINC (CAVATYIC) (BY SIMILARITY).  
 FT ACT\_SITE 226 226 BY SIMILARITY.  
 FT METAL 229 229 ZINC (CAVATYIC) (BY SIMILARITY).  
 FT METAL 235 235 ZINC (CAVATYIC) (BY SIMILARITY).  
 FT DISULFID 295 482 BY SIMILARITY.  
 SQ SEQUENCE 482 AA; 54373 MW; 366149FAF2BDC8BB CRC64;

Query Match 29.1%; Score 49.5; DB 1; Length 482;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Oy 9 VYSRIPO-PLPFINSYFQY 27  
 ||:|||||:|:|  
 Db 397 VILREPTLFFVGEYYSY 416

Search completed: March 9, 2002, 00:47:35  
 Job time: 796 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:48 ; Search time 94.88 Seconds  
(without alignments)  
46.250 Million cell updates/sec

Title: US-09-922-067-2

Perfect score: 170

Sequence: 1 WHPPLGDEVYSRIQPLFFINSEYFQVPAN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	96	56.5	346	11 Q9DB74	Q9db74 mus musculus
2	57	33.5	384	5 O44753	O44753 caenorhabdi
3	56	32.9	1183	3 Q9HDY4	Q9hdy4 schizosacch
4	54	31.8	872	4 Q9P221	Q9p221 homo sapien
5	52	30.6	215	1 O58800	O58800 pyrococcus
6	52	30.6	1038	2 O45780	O45780 bacteroides
7	52	30.6	2785	4 O75691	O75691 homo sapien
8	51.5	30.3	1253	6 O97566	O97566 canis famil
9	51	30.0	182	10 P93190	P93190 hordeum vul
10	51	30.0	864	10 Q9AXG8	Q9axg8 zea mays (m
11	50.5	29.7	835	3 Q02725	Q02725 saccharomyc
12	50	29.4	246	11 Q9D8N6	Q9d8n6 mus musculu
13	50	29.4	274	11 O35590	O35590 myocastor c
14	50	29.4	654	5 Q9VFX6	Q9vfx6 dirosophila
15	50	29.4	728	3 Q9HFN3	Q9hfn3 candida tro
16	49.5	29.1	583	2 Q9PEU9	Q9peu9 xylella fas
17	49.5	29.1	1509	11 Q61194	Q61194 mus musculu
18	49.5	29.1	1658	11 Q61182	Q61182 mus musculu
19	49	28.8	139	11 Q9CSG5	Q9csg5 mus musculu

20	49	28.8	399	10 Q41695	Q41695 phaseolus a
21	49	28.8	489	2 Q9RRK7	Q9rrk7 deinococcus
22	49	28.8	600	2 Q9CEK0	Q9cek0 lactococcus
23	49	28.8	735	10 Q9FX21	Q9fx21 arabidopsis
24	49	28.8	858	10 Q9ZU05	Q9zu05 persea amer
25	48.5	28.5	91	12 Q93666	Q93666 paramecium
26	48	28.2	216	2 Q9KXC0	Q9kxc0 escherichia
27	48	28.2	216	9 Q9XJK7	Q9xjk7 bacterioph
28	48	28.2	546	2 Q07713	Q07713 staphylococ
29	48	28.2	690	5 Q9XWC5	Q9xwc5 caenorhabdi
30	48	28.2	726	2 Q9X839	Q9x839 streptomyce
31	47.5	27.9	290	5 Q9NGH8	Q9ngh8 tripeustes
32	47.5	27.9	316	2 Q9ABX5	Q9abx5 caulobacter
33	47.5	27.9	324	13 Q93507	Q93507 brachydanio
34	47.5	27.9	1155	2 Q9KQW2	Q9kqw2 vibrio chol
35	47.5	27.9	1604	3 Q14148	Q14148 schizosacch
36	47	27.6	255	2 Q9R9L8	Q9r9l8 rhizobium m
37	47	27.6	323	5 Q9N7R6	Q9n7r6 leishmania
38	47	27.6	332	2 Q9EX11	Q9ex11 streptomyce
39	47	27.6	388	4 Q95728	Q95728 homo sapien
40	47	27.6	448	13 Q99293	Q99293 xenopus lae
41	47	27.6	503	2 Q9I362	Q9i362 pseudomonas
42	47	27.6	558	10 Q9M175	Q9m175 arabidopsis
43	47	27.6	662	1 Q9HI06	Q9hi06 halobacteri
44	47	27.6	706	1 Q52000	Q52000 halobacteri
45	47	27.6	734	6 Q9BEG8	Q9beg8 bos taurus

## ALIGNMENTS

RESULT 1

Q9DB74	Q9DB74	PRELIMINARY;	PRT;	346 AA.
AC	Q9DB74			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	PHOSPHOLIPASE A2 GROUP VII (PLATELET-ACTIVATING FACTOR)			
DE	ACETYLHYDROLASE, PLASMA).			
GN	PLA2G7			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
FN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=CEREBELLUM;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK005158; BAB23849.1;			
DR	MGI; MGI:1351327; pla2g7.			
DR	InterPro; IPR000379; Est_lip_thioest_actsite.			
DR	InterPro; IPR000734; Lipase.			

ID 058800 PRELIMINARY; PRT; 215 AA.

01-MAR-2001 (TREMBLrel. 16, Created)



```
O75691          PRELIMINARY;      PRT;   2785 AA..
ID              AC075691;
AC              O75691;
DT              01-NOV-1998 (TREMBLrel. 08, Created)
DI              DT              01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DR              DT              01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE              DRIM PROTEIN.
GN              DRIM.
OS              Homo sapiens (Human).
OC              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxId=9606;
RN              [1]
SQ              SEQUENCE FROM N.A.
RX              MEDLINE=98338066; PubMed=9673349;
RA              Schwärzke M., Gnirke A., Bork P., Tarin D., Weidle U.H.;
RT              Differential gene expression in mammary carcinoma cell lines;
RL              Identification of DRIM, a new gene down-regulated in metastasis.";
RR              Anticancer Res. 18:1409-1421(1998).
DR              ENBL; AJ006778; CAA07243.1; -.
FC              CONFLICT    1505     1505        P -> A (IN REF. I.).
SQ              SEQUENCE    2785 AA; 318423 MW;  6A2BBE9E8AD39683 CRC64.
```

```

Query Match          30.6%; Score 52; DB 4; Length 2785;
Best Local Similarity 53.3%; Pred.No. 1.9e+02;
Matches 16; Conservative 2; Mismatches 8; Indels 4; Gaps 2;

QY      3  FPLGDEVYSRIPOQLF--FINSEVFQYPPAN 30
      ||  ||  ||  ||  ||  ||  ||  ||
DB      831  FPERVEPRSRKLSPLFRFINNVE--vPAD 858

```

RESULT	8	
097566		
ID	097566	PRELIMINARY;
AC	097566;	PRT; 1253 AA.
DT	01-MAY-1999	(TREMBlrel. 10, Created)
DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)
DT	01-JUN-2001	(TREMBlrel. 17, Last annotation update)
DE	ALPHA-1 TYPE VII COLLAGEN NON-COLLAGENOUS DOMAIN (FRAGMENT).	
GN	COL7AL.	
OS	Canis familiaris (Dog).	

OC	Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Canidae; Canis.
OX	NCBI_TaxID=9615;
ON	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99002915; PubMed=9784596;
RA	Xu L., Chen M., Peng J., O'Toole E.A., Woodley D.T., Chan L.S.;
RT	"Molecular cloning and characterization of a cDNA encoding canine type
RT	VII collagen non-collagenous (NC1) domain, the target antigen of
RT	autoimmune disease epidermolysis bullosa acquisita (EBA).";
RL	Biochim. Biophys. Acta 1408:25-34(1998).
RL	EMBL; AF042093; AAC72024.1; -.
DR	HSSP; P02751; 1FNA.
DR	InterPro; IPR003962; FNIII_repeat.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR002035; VWFA.
DR	Pfam; PF00041; fn3; 9.
DR	Pfam; PF00092; vwa; 2.
DR	PRINTS; PR00014; FNTPR111.
DR	PRINTS; PR00453; VWFADOMAIN.
DR	SMART; SM00060; FN3; 9.
DR	SMART; SM00327; VWA; 2.
DR	PROSITE; PS50234; VWFA; 2.
KW	Collagen; Repeat.
FT	NON_TER 1253
FT	SEQUENCE 1253 AA; 133695 MW; 7FF2B500E4B8CA99 CRC64;

Query Match	30.3%	Score 51.5;	DB 6;	Length 1253;
Best Local Similarity	42.9%	Pred. No. 93;		

Query Match 30.0%; Score 51; DB 10; Length 864;

RL Submitted (SEP-1997) to the EMBL/GenBank

Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U36624; AAB68168.1; -  
 DR SGD; S0005940; VTC3.  
 DR InterPro; IPR001917; AminoTransf\_2.  
 DR InterPro; IPR001064; Crystallin.  
 DR PROSITE; PS00599; AA\_TRANSFER\_CLASS\_2; UNKNOWN\_1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 SQ SEQUENCE 835 AA; 95553 MW; F098B36A9D9B9C11 CRC64;

Query Match 29.7%; Score 50.5; DB 3; Length 835;  
 Best Local Similarity 43.5%; Pred. No. 83;  
 Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 7 DEVYSRIPQPLFFINS-EYFOYP 28  
 I : I I I I I : I I I I I  
 Db 466 DDIDSINPNPLRFLRAGEYSKFP 488

## RESULT 12

ID Q9DBN6 PRELIMINARY; PRT; 246 AA.  
 AC Q9DBN6;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE 1810054G18RIK PROTEIN.  
 GN 1810054G18RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Akaiwa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kouchiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Roffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.  
 FT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 405:685-690(2001).  
 DR EMBL; AK007858; BAB25310.1; -  
 DR MGD; MGI:1922910; 1810054G18RIK.  
 SQ SEQUENCE 246 AA; 28378 MW; 6FD6104D9945A81D CRC64;

Query Match 29.4%; Score 50; DB 11; Length 246;  
 Best Local Similarity 71.4%; Pred. No. 26;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PLGDVSRIPQPL 17  
 I I I I I I I I I I I  
 Db 171 PLGDACRSRIPSPL 184

## RESULT 13

Q35590 PRELIMINARY; PRT; 274 AA.  
 ID Q35590  
 AC Q35590;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE LECITHIN:CHOLESTEROL ACYL TRANSFERASE (FRAGMENT).  
 GN LCAT.  
 OS Myocastor coypus (Coypu) (Nutria).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;  
 ON NCBI\_TaxID=10157;  
 RN [1]

SEQUENCE FROM N.A.

RA Robinson M., Catzefflis F.M., Briolay J., Mouchiroud D.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U72324; AAB60792.1; -  
 DR EMBL; U72323; AAB60792.1; JOINED.  
 DR InterPro; IPR000734; Lipase.  
 DR InterPro; IPR003386; LACT.  
 DR Pfam; PF02450; LACT; 1.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Transferase.  
 FT NON\_TER 1 274  
 FT NON\_TER 274  
 SQ SEQUENCE 274 AA; 31979 MW; 29F87D1C5FF5B352 CRC64;

Query Match 29.4%; Score 50; DB 11; Length 274;

Best Local Similarity 44.4%; Pred. No. 29;

Matches 12; Conservative 6; Mismatches 5; Indels 4; Gaps 2;

QY 1 WMFPLGDEVYSRIPQPLFFINSYFOY 27  
 I I I I I : I I I I I I  
 Db 155 WMFPL-NQW---PESHVFISQDFNY 177

## RESULT 14

ID Q9VFX6 PRELIMINARY; PRT; 654 AA.  
 AC Q9VFX6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CG8449 PROTEIN.  
 GN CG8449.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20195006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champ M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003699; AAF54919.1; .  
DR FlyBase; FBgn0038129; CG8449.  
DR InterPro; IPR000195; RABGAP\_TBC.  
DR Pfam; PF00566; TBC; 1.  
DR SMART; SM00164; TBC; 1.  
SQ SEQUENCE 654 AA; 74337 MW; 27D1C3339B02A597 CRC64;

Query Match 29.4%; Score 50; DB 5; Length 654;  
Best Local Similarity 32.1%; Pred. No. 75;  
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 3 FPLGDEVSRIPQPLFFINSEYFQYPAN 30  
Db 383 YPNVDVHLVRLHALFNLNPKQFEXPPN 410

RESULT 15  
Q9HFN3 PRELIMINARY; PRT; 728 AA.  
AC Q9HFN3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK RELATED PROTEIN HSRL.  
GN HSRL.  
OS Candida tropicalis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5482;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Serrano R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ali R., Pascual-Ahuir A., Marquez J.A., Malik K.A.;  
RT "Identification of *Candida tropicalis* HSRL, a gene of the heat-shock  
RT factor related family which confers salt tolerance in *Saccharmyces  
RT cerevisiae*.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ296093; CAC12663.1; .  
DR InterPro; IPR000232; HSF\_DNA\_bind.  
DR InterPro; IPR002341; HSF\_ETs.  
DR Pfam; PF00447; HSF\_DNA\_bind; 2.  
DR PRINTS; PR00056; HSFDOMAIN.  
DR PRINTS; PR01217; PRICHEXTENSIN.  
DR ProDom; PD001788; HSF\_DNA\_bind; 1.  
DR SMART; SM00415; HSF; 1.  
DR PROSITE; PS00434; HSF\_DOMAIN; 1.  
SQ SEQUENCE 728 AA; 80664 MW; 13D53EB4AB3AB87A CRC64;

Query Match 29.4%; Score 50; DB 3; Length 728;

Best Local Similarity 42.1%; Pred. No. 85;  
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 12 RIQPLFFINSEYFQYPAN 30  
Db 249 QLPTPQPVYQGVYQYVPGS 267

Search completed: March 9, 2002, 00:46:51  
Job time: 827 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 Seconds  
(without alignments)  
12.292 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101

Sequence: 1 WLMGNILRLFLGSMTPAN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

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22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	440	22	AAE00782
2	101	100.0	440	22	AAE00783
3	101	100.0	441	16	AAE00784
4	101	100.0	441	16	AAE00785
5	101	100.0	441	16	AAE00786
6	101	100.0	441	16	AAE00787
7	101	100.0	441	16	AAE00788
8	101	100.0	441	16	AAE00789
9	101	100.0	441	16	AAE00790
10	101	100.0	441	16	AAE00791
11	101	100.0	441	16	AAE00792

12	101	100.0	441	16	AAE00793
13	101	100.0	441	16	AAE00794
14	101	100.0	441	16	AAE00795
15	101	100.0	441	16	AAE00796
16	101	100.0	441	16	AAE00797
17	101	100.0	441	16	AAE00798
18	101	100.0	441	16	AAE00799
19	101	100.0	441	16	AAE00800
20	101	100.0	441	16	AAE00801
21	101	100.0	441	16	AAE00802
22	101	100.0	441	16	AAE00803
23	101	100.0	441	16	AAE00804
24	101	100.0	441	16	AAE00805
25	101	100.0	441	16	AAE00806
26	101	100.0	441	16	AAE00807
27	101	100.0	441	16	AAE00808
28	101	100.0	441	16	AAE00809
29	101	100.0	441	16	AAE00810
30	101	100.0	441	16	AAE00811
31	101	100.0	441	16	AAE00812
32	101	100.0	441	16	AAE00813
33	101	100.0	441	16	AAE00814
34	101	100.0	441	16	AAE00815
35	101	100.0	441	16	AAE00816
36	101	100.0	441	16	AAE00817
37	101	100.0	441	16	AAE00818
38	101	100.0	441	16	AAE00819
39	101	100.0	441	16	AAE00820
40	101	100.0	441	16	AAE00821
41	101	100.0	441	16	AAE00822
42	91	90.1	193	16	AAE00823
43	91	90.1	193	16	AAE00824
44	91	90.1	193	16	AAE00825
45	91	90.1	193	16	AAE00826

#### ALIGNMENTS

RESULT 1

AAE00782

ID AAE00782 standard; Protein; 440 AA.

AC AAE00782;

XX 02-JUL-2001 (first entry)

DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHCL.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;  
KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..97

FT /note= "Corresponds to N-terminal 97 amino acids of mouse  
plasma platelet-activating factor acetylhydrolase  
(PAF-AH)"

FT 98..440

FT /note= "Corresponds to C-terminal 343 amino acids of  
human plasma platelet-activating factor acetylhydrolase  
(PAF-AH)"

US6203790-B1.

PD 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.







PT New nucleic acid encoding platelet activating factor.  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLGSMTPAN 19  
 DB 115 wlmgnilrlflgsmtpan 133

# RESULT 6

AAR71920  
 ID AAR71920 standard; Protein; 441 AA.

AC AAR71920;

DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S108A.

DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

DR WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given

CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLGSMTPAN 19  
 DB 115 wlmgnilrlflgsmtpan 133

# RESULT 7

AAR71921  
 ID AAR71921 standard; Protein; 441 AA.

AC AAR71921;

DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S273A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetylhydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTTPAN 19  
 |||  
 DB 115 wlmgnilrlfsgmttpan 133

RESULT 8  
 AAR71922  
 ID AAR71922 standard; Protein; 441 AA.  
 XX  
 AC AAR71922;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant D296A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 296 /note= "Wild-type Asp is substd. by Ala."  
 FT  
 XX  
 PN W09509921-A.  
 XX  
 PD 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; : 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTTPAN 19  
 |||  
 DB 115 wlmgnilrlfsgmttpan 133

RESULT 9  
 AAR71924  
 ID AAR71924 standard; Protein; 441 AA.  
 XX  
 AC AAR71924;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant H351A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

AAR71923  
 ID AAR71923 standard; Protein; 441 AA.  
 XX  
 AC AAR71923;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant D338A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 338 /note= "Wild-type Asp is substd. by Ala."  
 FT  
 XX  
 PN W09509921-A.  
 XX  
 PD 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; : 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTTPAN 19  
 |||  
 DB 115 wlmgnilrlfsgmttpan 133

RESULT 10  
 AAR71924  
 ID AAR71924 standard; Protein; 441 AA.  
 XX  
 AC AAR71924;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant H351A.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

KW disease; pleurisy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 351  
/note= "Wild-type His is substd. by Ala."

XX W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetylhydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73045-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLIFGSMTPAN 19

DB 115 wlmgnilrlifgsmttpan 133

RESULT 11

AAR71925  
ID AAR71925 standard; Protein; 441 AA.

XX AC AAR71925;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant H395A/H399A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 395  
/note= "Wild-type His is substd. by Ala."

FT 399

FT /note= "Wild-type His is substd. by Ala."

XX

PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetylhydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLIFGSMTPAN 19

DB 115 wlmgnilrlifgsmttpan 133

RESULT 12

AAR73046  
ID AAR73046 standard; Protein; 441 AA.

XX AC AAR73046;

XX DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C67S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 67  
/note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.



Search completed: March 9, 2002, 00:31:57  
Job time: 443 sec

RESULT	15	
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ID	AAW26498	standard; Protein; 441 AA.
XX	XX	
AAW26498;		
XX	XX	
DT	05-JAN-1998	(first entry)
XX	XX	
DE	XX	
DE	XX	Human platelet-activating factor acetylhydrolase.
KW	XX	
KW	XX	Platelet-activating factor acetylhydrolase; PAF-AH; human;
KW	XX	inflammation; asthma; pleurisy; necrotising enterocolitis;
KW	XX	adult respiratory distress syndrome; therapy.

ID	AAW26498 standard; Protein; 441 AA.
AAW26498	standard; Protein; 441 AA.

XX

platelet-activating factor acetylhydrolase; PAF-AH; human;  
inflammation; asthma; pleurisy; necrotising enterocolitis;  
adult respiratory distress syndrome; therapy.

XX

PD 12-AUG-1997.

PF 06-OCT-1993; 93US-0133803.  
XX

PR 06-OCT-1993; 93US-0133803.

PA (ICOS-) ICOS CORP.

PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
PI Wilder CJ.

DR WPI; 1997-

## PT Detecting lesions

PS Example 3; Column 47-50; 53pp; English.

This polypeptide comprises human plasma platelet-activating factor acetylhydrolase (PAF-AH), a protein that inactivates PAF and inactivates oxidatively fragmented phospholipids such as products of the arachidonic acid cascade that mediate inflammation. Its sequence was deduced from a full-length cDNA Clone (see AAT87048) obtained from a macrophage cDNA library. Mouse, dog, cattle, chicken, rat and macaque PAF-AH polypeptides (see AAT26500-505) have also been identified. Recombinant PAF-AH polypeptides can be produced in prokaryotic or eukaryotic host cells and used to mimic or augment normal processes of resolution of inflammation *in vivo*. Examples describe the *in vivo* therapeutic effect of recombinant PAF-AH products on acute inflammation, pleurisy, asthma, necrotising enterocolitis and adult respiratory distress syndrome in animal models.

Query Match	100.0%;	Score 101;	DB 18;	Length 441;
Best Local Similarity	100.0%;	pred. No. 6.2e-10;		

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

115 wingnrrlltgsmttpan 133

us-09-922-067-4.rag

• Mon Mar 11 10:02:06 2002





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:32:59 ; Search time 47.03 seconds  
(without alignments)  
9.091 Million cell updates/sec

Title: US-09-922-067-4  
Perfect score: 101

Sequence: 1 WLMGNILRLFGSMTPAN 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	19	2	US-08-557-892-4
2	101	100.0	19	2	US-08-387-858A-4
3	101	100.0	19	4	US-09-294-334B-4
4	101	100.0	441	1	US-08-470-187-8
5	101	100.0	441	1	US-08-318-905-8
6	101	100.0	441	1	US-08-483-232-8
7	101	100.0	441	1	US-08-483-140-8
8	101	100.0	441	2	US-08-485-938A-8
9	101	100.0	441	2	US-08-910-041-8
10	101	100.0	441	3	US-09-328-474-8
11	101	100.0	441	3	US-09-100-546-8
12	101	100.0	441	4	US-09-010-715-8
13	101	100.0	441	4	US-09-577-758-8
14	91	90.1	193	1	US-08-483-140-30
15	91	90.1	193	2	US-08-485-938A-36
16	77	76.2	444	1	US-08-483-140-28
17	77	76.2	444	2	US-08-485-938A-32
18	72	71.3	444	2	US-08-485-938A-33
19	68	67.3	440	1	US-08-483-140-27
20	68	67.3	440	2	US-08-485-938A-31
21	44	43.6	730	1	US-08-121-713D-58
22	44	43.6	730	1	US-08-835-268-58
23	44	43.6	730	2	US-09-060-692-58
24	44	43.6	730	3	US-08-833-391-58
25	44	43.6	730	5	PCT-US94-10151A-58
26	42	41.6	999	2	US-08-770-301A-1
27	42	41.6	999	3	US-09-175-581-1

Sequence 2, Appli  
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Sequence 2, Appli  
Sequence 12, Appli

28 42 41.6 1023 2 US-08-475-891A-2  
29 42 41.6 1023 2 US-08-567-375-2  
30 42 41.6 1023 2 US-08-587-680A-2  
31 40 39.6 347 1 US-08-118-270-47  
32 40 39.6 347 5 PCT-US93-08528-47  
33 40 39.6 363 1 US-08-148-209A-2  
34 40 39.6 363 1 US-08-148-209A-3  
35 40 39.6 1382 3 US-09-057-570-4  
36 40 39.6 1657 3 US-09-057-570-2  
37 40 39.6 1805 3 US-09-057-570-7  
38 39 38.6 313 3 US-08-926-842B-62  
39 39 38.6 377 3 US-09-150-133-5  
40 39 38.6 377 3 US-09-150-141-5  
41 39 38.6 377 4 US-09-374-493-5  
42 39 38.6 377 4 US-09-374-824-5  
43 39 38.6 377 4 US-09-374-492-5  
44 38 37.6 125 5 PCT-US93-06829-2  
45 38 37.6 125 5 PCT-US93-06829-12

#### ALIGNMENTS

RESULT 1  
US-08-557-892-4  
; Sequence 4, Application US/08557892  
; Patent No. 5968818  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloyer, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557,892  
; FILING DATE: 14 No. 5968818member 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,858  
; FILING DATE: 14 No. 5968818member 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; US-08-557-892-4

Query Match 100.0%; Score 101; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSWTTPAN 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 WLMGNILRLFLFGSWTTPAN 19

## RESULT 2

US-08-387-858A-4  
; Sequence 4, Application US/08397858A  
; Patent No. 5981252  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387-858A  
; FILING DATE: 24 February 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/01374  
; FILING DATE: 24 June 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:

INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-387-858A-4

Query Match 100.0%; Score 101; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSWTTPAN 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 WLMGNILRLFLFGSWTTPAN 19

## RESULT 3

US-09-294-384B-4  
; Sequence 4, Application US/09294384B  
; Patent No. 6177257  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,384B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,858  
; FILING DATE: 24 February 1995  
; APPLICATION NUMBER: PCT/GB94/01374  
; FILING DATE: 24 June 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:

INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-09-294-384B-4

Query Match 100.0%; Score 101; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSWTTPAN 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 WLMGNILRLFLFGSWTTPAN 19

## RESULT 4

US-08-470-187-8  
; Sequence 8, Application US/08470187  
; Patent No. 5532152  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine E.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl

```

; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-187-8

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Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WLMGNILRLFGSMTTPAN 19
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Db 115 WLMGNILRLFGSMTTPAN 133

```

```

RESULT 5
US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-905-8

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```

Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WLMGNILRLFGSMTTPAN 19
   ||||||||||||||||
Db 115 WLMGNILRLFGSMTTPAN 133

```

```

RESULT 6
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-232-8

Query Match 100.0%; Score 101; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTPAN 19  
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 7  
US-08-483-140-8  
Sequence 8, Application US/08483140  
Patent No. 5698403  
GENERAL INFORMATION:  
APPLICANT: ICOS Corporation  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,140  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 6-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5698403and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-140-8

Query Match 100.0%; Score 101; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTPAN 19  
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 8  
US-08-485-938A-8  
Sequence 8, Application US/08485938A  
Patent No. 5847088  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tioelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,938A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5847088and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32792  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-938A-8

Query Match 100.0%; Score 101; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTPAN 19  
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 9  
US-08-910-041-8  
Sequence 8, Application US/08910041  
Patent No. 5977308  
GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,041  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,232  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27866/34026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-910-041-8

Query Match 100.0%; Score 101; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTTPAN 19  
DB 115 WLMGNILRLFGSMTTPAN 133

RESULT 10  
US-09-328-474-8  
Sequence 8, Application US/09328474  
Patent No. 6045794  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/328,474  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,232  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27866/34026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-328-474-8

Query Match 100.0%; Score 101; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTTPAN 19  
DB 115 WLMGNILRLFGSMTTPAN 133

RESULT 11  
US-09-100-546-8  
Sequence 8, Application US/09100546  
Patent No. 6099836  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,546  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 609836and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-100-546-8

Query Match 100.0%; Score 101; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLGSMTPAN 19  
Db 115 WLMGNILRLFLGSMTPAN 133

RESULT 12  
US-09-010-715-8  
Sequence 8, Application US/09010715  
Patent No. 6146625  
GENERAL INFORMATION:  
APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6146625and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-010-715-8

Query Match 100.0%; Score 101; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLGSMTPAN 19  
Db 115 WLMGNILRLFLGSMTPAN 133

RESULT 13  
US-09-577-758-8  
Sequence 8, Application US/09577758  
Patent No. 6203790  
GENERAL INFORMATION:  
APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/577,758  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/010,715  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6203790and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-577-758-8

Query Match 100.0%; Score 101; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19  
||||| ||||| |||||  
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 14  
US-08-483-140-30

; Sequence 30, Application US/08483140  
; Patent No. 5698403  
; GENERAL INFORMATION:  
; APPLICANT: ICOS Corporation  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,140  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 6-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5698403and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-140-30

Query Match 90.1%; Score 91; DB 1; Length 193;  
Best Local Similarity 89.5%; Pred. No. 1.4e-08;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19  
||||| ||||| |||||  
Db 73 WLMGNILRLFGSMTPAN 91

RESULT 15

US-08-485-938A-36  
; Sequence 36, Application US/08485938A  
; Patent No. 5847088

; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,938A  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5847088and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32792  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-938A-36

Query Match 90.1%; Score 91; DB 2; Length 193;  
Best Local Similarity 89.5%; Pred. No. 1.4e-08;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19  
||||| ||||| |||||  
Db 73 WLMGNILRLFGSMTPAN 91

Search completed: March 9, 2002, 00:33:00  
Job time: 401 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:10 ; Search time 53.53 seconds  
(without alignments)  
27.037 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101  
Sequence: 1 WLMGNILRLFGSMTPAN 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	101	100.0	441	2 S60247	platelet-activatin
2	48	47.5	436	2 JC5021	platelet-activatin
3	46	45.5	410	2 D83923	spore germination
4	45.5	45.0	247	2 S59523	triose-phosphate i
5	45	44.6	417	2 D82111	uracil permease VC
6	44	43.6	122	2 T16624	hypothetical prote
7	44	43.6	448	2 A26190	gluconate permease
8	44	43.6	730	2 JH0798	fasciclin IV precu
9	43	42.6	185	2 H72259	ribosome recycling
10	43	42.6	422	2 S74581	hypothetical prote
11	43	42.6	836	2 D82177	conserved hypotet
12	42.5	42.1	403	2 D75333	conserved hypotet
13	42	41.6	422	2 G83503	probable MFS trans
14	42	41.6	476	2 H96802	probable amino aci
15	42	41.6	999	2 JC5278	oxygen-regulated p
16	41	40.6	266	2 P83741	hypothetical prote
17	41	40.6	308	1 H65050	probable ATP-bindi
18	41	40.6	308	2 D85919	hypothetical prote
19	41	40.6	338	2 S24930	hypothetical prote
20	41	40.6	444	2 G69905	gluconate permease
21	41	40.6	448	2 JC2305	annexin - chicken
22	41	40.6	671	2 JC2029	hypothetical prote
23	41	40.6	1817	2 T34249	triose-phosphate i
24	40.5	40.1	247	2 S18604	hypothetical prote
25	40	39.6	123	2 H72698	hypothetical prote
26	40	39.6	204	2 S07786	hypothetical prote
27	40	39.6	233	2 T24714	hypothetical prote
28	40	39.6	251	2 T40671	fliR protein - Cau
29	40	39.6	256	2 T24713	hypothetical prote

30 40 39.6 278 2 S64317 probable membrane  
31 40 39.6 316 2 T00769 hypothetical prote  
32 40 39.6 363 2 T48261 angiotensin II rec  
33 40 39.6 363 2 A49092 angiotensin II rec  
34 40 39.6 363 2 JC2543 uracil permease PA  
35 40 39.6 427 2 E83066 probable lipopolys  
36 40 39.6 432 2 F71152 ntpi protein - Ent  
37 40 39.6 664 2 B53610 hypothetical prote  
38 40 39.6 1098 2 B70232 hypothetical prote  
39 40 39.6 1107 2 T25450 hypothetical prote  
40 40 39.6 1345 2 S46817 probable nucleopor  
41 40 39.6 1778 2 T50074 W0R1 protein - yea  
42 39.5 146 2 S22775 conserved hypotet  
43 39.5 146 2 F82048 conserved hypotet  
44 39.5 240 2 B82833 conserved hypotet  
45 39 38.6 165 2 F81734 conserved hypotet

#### ALIGNMENTS

##### RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Rjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g780133

Query Match 100.0%; Score 101; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19

Db 115 WLMGNILRLFGSMTPAN 133

##### RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C>Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, C.

J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KARI>

A:Cross-references: DDBJ:D67037; NID:gl644228; PIDN:BA11054.1; PID:gl644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>

F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted



A:Molecule type: DNA  
A:Residues: 1-448 <FUJ>  
A:Cross-references: GB:AB005554; GB:D45242; GB:D31629; NID:g2280496; PIDN:BAAL1577.1; PID:916565  
C:Species: *Thermotoga maritima*  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet  
C:Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho  
A: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabet, C.; Ferrari, E.  
Nature 330, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Galled  
iech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
ateuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, K.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Darchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A:Reference number: A69580; MUID:96044033  
A:Accession: D69636  
A:Molecule type: DNA  
A:Residues: 1-448 <KUN>  
A:Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16044.1; PID:g2636554  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: gntP  
C:Superfamily: D-serine permease  
C:Keywords: transmembrane protein

Query Match 43.6%; Score 44; DB 2; Length 448;  
Best Local Similarity 50.0%; Pred. No. 15;  
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 1 WLMGNTLRLLFGSMTPPA 18  
DB 351 WLIAAILRLISLGSATVAA 368  
RESULT 8  
fasciclin IV precursor - American bird grasshopper  
C:Species: *Schistocerca americana* (American bird grasshopper)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: JH0798  
R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good  
Neuron 9, 831-845, 1992  
A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in  
A:Reference number: JH0798; MUID:93040225  
A:Accession: JH0798  
A:Molecule type: mRNA  
A:Residues: 1-730 <KOL>  
A:Cross-references: GB:L00709; NID:g160844; PID:g160845  
A:Experimental source: embryo  
C:Comment: This protein plays a role in growth cone guidance in the developing central r  
C:Keywords: glycoprotein; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-730/Product: fasciclin IV #status predicted <WAT>  
F:23-627/Domain: extracellular #status predicted <EXT>  
F:628-652/Domain: transmembrane #status predicted <TMM>  
F:653-730/Domain: intracellular #status predicted <INT>  
F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.6%; Score 44; DB 2; Length 730;  
Best Local Similarity 43.8%; Pred. No. 24;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 4 GNTLRLLFGSMTPPAN 19  
DB 294 GQVEKLYGVFTTPVN 309

RESULT 9  
H72259  
ribosome recycling factor - *Thermotoga maritima* (strain MS88)  
C:Species: *Thermotoga maritima*  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: H72259  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316  
A:Accession: H72259  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-185 <ARN>  
A:Cross-references: GB:AE001792; GB:AE000512; NID:g4981952; PIDN:AAD36470.1; PID:g498  
A:Experimental source: strain MS88  
C:Genetics:  
A:Gene: TMI399  
C:Superfamily: ribosome releasing factor

Query Match 42.6%; Score 43; DB 2; Length 185;  
Best Local Similarity 61.5%; Pred. No. 8.4;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 4 GNTLRLLFGSMTP 16  
DB 95 GNVRLVFPSPPT 107

RESULT 10  
S74581  
hypothetical protein slr1411 - *Synechocystis* sp. (strain PCC 6803)  
C:Species: *Synechocystis* sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S74581  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*  
S:Reference number: S74322; MUID:97061201  
A:Accession: S74581  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-422 <KAN>  
A:Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAAL16733.1; PID:g165  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH1109

Query Match 42.6%; Score 43; DB 2; Length 422;  
Best Local Similarity 52.9%; Pred. No. 20;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 3 GNTLRLLFGSMTPAN 19  
DB 238 LANILRLWIGTTPHN 254

RESULT 11  
DB2177  
conserved hypothetical protein VC1629 [imported] - *Vibrio cholerae* (strain N16961 se  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: DB2177  
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Seller  
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Query Match 41.6%; Score 42; DB 2; Length 999;

Best Local Similarity 53.3%; Pred. No. 74;  
Matches 8; Conservative 2; Mismatches

5; Indels 0; Gaps 0;

OY 3 MGNILRLFGSWTTP 17

:||: ||| |||

DB 577 LGNTISSLFGGGTTP 591

Search completed: March 9, 2002, 00:34:11  
Job time: 322 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:35 ; Search time 30.16 seconds  
(without alignments)  
23.098 Million cell updates/sec

Title: US-09-922-067-4  
Perfect score: 101  
Sequence: 1 WLMGNILRLIFGSMTPAN 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	441	1 PAPA_HUMAN	QJ3093 h platelet-
2	77	76.2	444	1 PAPA_CANFA	Q28262 c platelet-
3	72	71.3	444	1 PAPA_BOVIN	Q28017 b platelet-
4	68	67.3	440	1 PAPA_MOUSE	Q60963 m platelet-
5	48	47.5	436	1 PAPA_GAVPO	P70683 c platelet-
6	45.5	45.0	250	1 TPIS_GRAVE	P48492 gracilaria
7	44	43.6	448	1 GNTP_BACSU	P12012 bacillus su
8	44	43.6	730	1 SMIA_SCHAM	Q26473 schistocerc
9	43	42.6	185	1 OXRP_THEMA	Q9Y411 homo sapien
10	42	41.6	999	1 OXRP_HUMAN	Q9Y411 homo sapien
11	41	40.6	321	1 GUTQ_ECOLI	P17115 escherichia
12	41	40.6	338	1 Y38K_CORSE	Q39635 corydalis s
13	41	40.6	444	1 YQJA_BACSU	Q31862 bacillus su
14	41	40.6	448	1 GNTP_BACLI	P46832 bacillus li
15	41	40.6	618	1 ANX6_BOVIN	P79134 bos taurus
16	41	40.6	671	1 ANX6_CHICK	P51901 gallus gall
17	40.5	40.1	247	1 YBGT_DRONE	P29613 drosophila
18	40	39.6	277	1 YBGT_ECOLI	P56100 escherichia
19	40	39.6	204	1 YPOB_STYLE	P14289 stylonychia
20	40	39.6	251	1 FLIR_CAUCR	P45975 caulobacter
21	40	39.6	278	1 YG11_YEAST	P53217 saccharomyc
22	40	39.6	363	1 AG22_HUMAN	P50052 homo sapien
23	40	39.6	363	1 AG22_MERUN	Q9Z026 meriones un
24	40	39.6	363	1 AG22_MOUSE	P35374 mus musculu
25	40	39.6	363	1 AG22_RAT	P35351 rattus norv
26	40	39.6	664	1 NTP1_ENTHR	P43439 enterococcu
27	40	39.6	1345	1 YHO0_YEAST	P38800 saccharomyc
28	40	39.6	1867	1 MOT1_YEAST	P32233 saccharomyc
29	39	38.6	120	1 CHH1_PENMO	O97383 penaeus mon
30	39	38.6	377	1 TPS2_HUMAN	O60704 homo sapien
31	39	38.6	414	1 URAA_HAEIN	P45117 haemophilus
32	39	38.6	457	1 SVC1_RICPR	Q9Z662 rickettsia
33	39	38.6	672	1 ANX6_HUMAN	P08133 homo sapien

RESULT 1

ID	PAPA_HUMAN	STANDARD;	PRT;	441 AA.
AC	Q13093; Q15692;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)			
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED			
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE			
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).			
GN	PLA2G7 OR PAFAH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.			
RC	TISSUE=Myeloid;			
RC	MEDLINE=95214779; PubMed=7700381;			
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,			
RA	Schlimp B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,			
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;			
RT	"Anti-inflammatory properties of a platelet-activating factor			
RT	acetylhydrolase.";			
RL	Nature 374:549-553(1995).			
RL	[2]			
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Lymphoma;			
RC	MEDLINE=96197208; PubMed=8624782;			
RA	Tew D.G., Southern C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,			
RA	Moore K., Gloger I.S., Macphie C.H.;			
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-			
RT	associated, serine-dependent phospholipase involved in the oxidative			
RT	modification of low-density lipoproteins.";			
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).			
RL	[3]			
RP	MUTAGENESIS.			
RC	MEDLINE=96029630; PubMed=7592717;			
RA	Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,			
RA	Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,			
RA	Gray P.W.;			
RT	"Plasma platelet-activating factor acetylhydrolase is a secreted			
RT	phospholipase A2 with a catalytic triad.";			
RL	J. Biol. Chem. 270:25481-25487(1995).			
RL	[4]			
RP	VARIANT PHE-279.			
RC	MEDLINE=96259525; PubMed=8675689;			
RA	Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,			
RA	Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,			
RA	McIntyre T.M., Gray P.W., Prescott S.M.;			
RT	"Platelet-activating factor acetylhydrolase deficiency. A missense			
RT	mutation near the active site of an anti-inflammatory			
RT	phospholipase.";			
RL	J. Clin. Invest. 97:2784-2791(1996).			
RL	[5]			

PI4824 mus musculu  
P48037 rattus norv  
P34651 caenorhabdl  
P26446 gallus gall  
P48494 oryza sativ  
O07585 beccillus su  
P06466 e phosphati  
Q56738 vibrio sp.  
Q28929 ovis aries  
Q12094 saccharomyc  
O13155 homo sapien  
P75564 mycoplasma

672 1 ANX6\_MOUSE  
672 1 ANX6\_RAT  
824 1 YOT5\_CAEEL  
1011 1 TPOL\_CHICK  
253 1 TPIS\_ORYSA  
444 1 YHDP\_BACSU  
249 1 CDSA\_ECOLI  
251 1 TPIS\_VIBSA  
260 1 AG22\_SHEEP  
313 1 Y006\_YEAST  
320 1 MCA2\_HUMAN  
341 1 SYFA\_MYCPN

ALIGNMENTS

RP VARIANT PRE-279.  
 RA MEDLINE-98430412; PubMed-9759612;  
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,  
 RA "A mutation in plasma platelet-activating factor acetylhydrolase  
 RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not  
 RT for hypertension.";  
 RL Thromb. Haemost. 80:372-375(1998).  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H<sub>2</sub>O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS  
 CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT  
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY  
 CC RESPONSES.  
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC -----  
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 CC -----  
 CC EMBL: U20157; AAC50126.1; -;  
 CC EMBL: U24577; AAB04170.1; -;  
 CC MIM: 601690; -;  
 CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 CC PROSITE: PS00120; LIPASE\_SER: 1.  
 CC Hydrolyase; Lipid degradation; Glycoprotein; Signal.  
 CC SIGNAL 1 21  
 CC CHAIN 22 441  
 CC  
 CC ACT\_SITE 273 273 PLATELET-ACTIVATING FACTOR  
 CC ACT\_SITE 296 296 CHARGE RELAY SYSTEM.  
 CC ACT\_SITE 351 351 CHARGE RELAY SYSTEM.  
 CC CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 433 433 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE  
 CC VARIANT 279 279 PROTEIN).  
 CC  
 CC MUTAGEN 108 108 /FTIG-VAR\_004268.  
 CC S->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 CC S->A: LOSS OF ACTIVITY.  
 CC D->A: ALMOST NO ACTIVITY.  
 CC D->N: DIMINISHED ACTIVITY.  
 CC D->A: LOSS OF ACTIVITY.  
 CC D->N: LOSS OF ACTIVITY.  
 CC D->A: NO CHANGE IN ACTIVITY.  
 CC D->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 CC H->A: LOSS OF ACTIVITY.  
 CC V -> A (IN REF. 2).  
 CC SEQUENCE 441 AA; 50077 MW; 3BA95EA9EB094A57 CRC64;

Query Match 100.0%; Score 101; DB 1; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WLMGNILRLFLGSMTPPAN 19  
 Db 115 WLMGNILRLFLGSMTPPAN 133

RESULT 2

PAPA\_CANFA  
 ID PAPA\_CANFA STANDARD; PRT; 444 AA.  
 AC Q28262;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (PAF)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LIDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LIDL-PLA2) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_Taxid=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Spleen;  
 RX MEDLINE-96029630; PubMed-7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H<sub>2</sub>O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- SUBCELLULAR LOCATION: PLASMA.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 CC -----  
 CC EMBL: U34245; AAC48484.1; -;  
 CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 CC PROSITE: PS00120; LIPASE\_SER: 1.  
 CC Hydrolyase; Lipid degradation; Glycoprotein; Signal.  
 CC SIGNAL 1 21  
 CC CHAIN 22 444  
 CC  
 CC ACT\_SITE 274 274 PLATELET-ACTIVATING FACTOR  
 CC ACT\_SITE 297 297 ACETYLHYDROLASE.  
 CC ACT\_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC CARBOHYD 60 60 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 444 AA; 50136 MW; 814EFOAE3B074AC CRC64;  
 Query Match 76.2%; Score 77; DB 1; Length 444;  
 Best Local Similarity 73.7%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 WLMGNILRLFLGSMTPPAN 19  
 Db 115 WLMGNILRLFLGSMTPPAN 133  
 RESULT 3  
 ID PAPA\_BOVIN STANDARD; PRT; 444 AA.



Q28017;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Splice;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 CC -----  
 DR EMBL: U34247; AAC48483.1;  
 DR InterPro: IPR000379; EST\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 444  
 FT PLATELET-ACTIVATING FACTOR  
 FT ACETYLHYDROLASE.  
 FT ACT\_SITE 274 274  
 FT ACT\_SITE 297 297  
 FT ACT\_SITE 352 352  
 FT ACT\_SITE 352 352  
 FT CARBOHYD 60 60  
 FT CARBOHYD 200 200  
 FT CARBOHYD 424 424  
 FT CARBOHYD 434 434  
 FT CARBOHYD 444 444  
 FT SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;  
 Query Match 71.3%; Score 72; DB 1; Length 444;  
 Best Local Similarity 72.2%; Pred. No. 0.00016;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WLMGNILRLFLFGSMITPA 18  
 Db 115 WLVGKIMGLFGSMITPA 132  
 RESULT 4  
 ID PAF\_MOUSE STANDARD; PRT; 440 AA.

Q60963;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7 OR PAFAH.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
 RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
 RA Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 CC -----  
 DR EMBL: U34277; AAC52274.1;  
 DR MGD: MGI:1351327; Pla2g7.  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 440  
 FT PLATELET-ACTIVATING FACTOR  
 FT ACETYLHYDROLASE.  
 FT ACT\_SITE 272 272  
 FT ACT\_SITE 295 295  
 FT ACT\_SITE 350 350  
 FT ACT\_SITE 350 350  
 FT CARBOHYD 59 59  
 FT CARBOHYD 75 75  
 FT CARBOHYD 199 199  
 FT CARBOHYD 440 440  
 FT SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;  
 Query Match 67.3%; Score 68; DB 1; Length 440;  
 Best Local Similarity 66.7%; Pred. No. 0.00073;  
 Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LMGNILRLFLFGSMITPAN 19  
 Db 115 IVGNILHLGSLTTFAS 132  
 RESULT 5  
 ID PAF\_MOUSE STANDARD; PRT; 436 AA.

AC P70683;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACETHYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA2) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7 OR PAFH.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HARTLEY; TISSUE=Liver;  
 RX MEDLINE=97103479; PubMed=8947850;  
 RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,  
 RA Yokoyama K., Setaka M., Nojima S.;  
 RT "Cloning, expression and characterization of plasma  
 RT platelet-activating factor-acetylhydrolase from guinea pig.";  
 RL J. Biochem. 120:838-844(1996).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H<sub>2</sub>O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 CC -----  
 CC EMBL: D67037; BA01054.1; -  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER: 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 436 PLATELET-ACTIVATING FACTOR  
 FT ACETYLHYDROLASE.  
 FT ACT\_SITE 271 271 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 436 AA; 49062 MW; C359D96E392FF61 CRC64;  
 Query Match 47.5%; Score 48; DB 1; Length 436;  
 Best Local Similarity 50.0%; Pred. No. 1.6;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Qy 3 MGNTLRLLFGSMTPA 18  
 Db 117 LGKLLKLLYGSVKVPA 132  
 RESULT 6  
 TPIS\_GRAVE  
 ID TPIS\_GRAVE STANDARD; PRT; 250 AA.  
 AC P48492;  
 DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (EC 5.3.1.1) (TIM) (FRAGMENT).  
 GN TPIL.  
 OS Gracilaria verrucosa.  
 OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae; Gracilariaceae;  
 OC Gracilaria.  
 OX NCBI\_TaxID=2777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96120860; PubMed=8590477;  
 RA Zhou Y.H., Ragen M.A.;  
 RT "Cloning and characterization of the nuclear gene and cDNAs for  
 RT triosephosphate isomerase of the marine red alga Gracilaria  
 RT verrucosa.";  
 RL Curr. Genet. 28:317-323(1995).  
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-  
 CC ACETONE PHOSPHATE.  
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
 CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC  
 CC AND PLASTID.  
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: L38662; AB01378.1; -  
 DR HSP; P00936; IHTI.  
 DR InterPro: IPR000652; Trioseph\_isomrse.  
 DR Pfam: PF00121; TIM; 1.  
 DR PRODOM: PD001005; Trioseph\_isomrse; 1.  
 DR PROSITE: PS00171; TIM; 1.  
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 KW Pentose shunt.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 87 87 BY SIMILARITY.  
 FT ACT\_SITE 160 160 BY SIMILARITY.  
 SQ SEQUENCE 250 AA; 26686 MW; D800EFF452D4D9D CRC64;  
 Query Match 45.0%; Score 45.5; DB 1; Length 250;  
 Best Local Similarity 34.6%; Pred. No. 2.3;  
 Matches 9; Conservative 4; Mismatches 6; Indels 7; Gaps 1;  
 Qy 1 WLMGNI-----LRLFGSMTPAN 19  
 Db 186 WLANNVSPQVAASRILYGGVSPAN 211  
 RESULT 7  
 GNTF\_BACSU  
 ID GNTF\_BACSU STANDARD; PRT; 448 AA.  
 AC P12012;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE GLUCONATE PERMEASE.  
 GN GNTF.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87008613; PubMed=3020045;  
 RA Fujita Y., Fujita T., Miwa Y., Nishashi J., Aratani Y.;





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RP SEQUENCE OF 3-313 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190542; PubMed=2134185;
RA Yamada M., Yamada Y., Saier M.H. Jr.;
RT "Nucleotide sequence and expression of the gutQ gene within the
RL glucitol operon of Escherichia coli.";
RL DNA Seq. 1:141-145(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maynew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SUBUNIT: HOMODIMER (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE SIS FAMILY. GUTQ/KPSF SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 214.
CC
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CC
CC EMBL; X51361; CAA35745.1; ALT_FRAME.
CC EMBL; U29579; AAA69217.1; ALT_INIT.
CC EMBL; AE000354; AAC75750.1; ALT_INIT.
CC PIR; S10373; S10373.
CC PIR; A48429; A48429.
CC EcoGene; EG10973; gutQ.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR001347; SIS.
CC Pfam; PF00571; CBS; 2.
CC Pfam; PF01380; SIS; 1.
CC ATP-binding; Repeat; CBS domain; Complete proteome.
FT NP_BIND 49 54 ATP (POTENTIAL).
FT DOMAIN 201 255 CBS 1.
FT DOMAIN 267 319 CBS 2.
FT SEQUENCE 321 AA; 34031 MW; 85C31DFBD92F7B7C CRC64;

Query Match 40.6%; Score 41; DB 1; Length 321;
Best Local Similarity 42.1%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 1 WLMGNILRLFGSMTPAN 19
DB 254 WLWVG-----GALATPVN 266

RESULT 12
Y38K_CORSE STANDARD; PRT; 338 AA.
AC Q39635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 38.1 KDA PROTEIN.
OS Corydalis sempervirens (Pink corydalis) (Rock-harlequin).
OC Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; Ranunculales;
OC Papaveraceae; Magnoliophyta; eudicotyledons; Ranunculales;
OC NCBI_TaxID=3464;
RN [1]
RP SEQUENCE FROM N.A.

Schaller A.;
Thesis (1991), University of Bochum, Germany.
-!- SIMILARITY: BELONGS TO THE THERMONUCLEASE FAMILY.
CC
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CC
CC EMBL; X63595; CAA45139.1; -.
CC HSSP; P00644; ISND.
CC InterPro; IPR000080; SNase.
CC InterPro; IPR002071; Theronuclease.
CC Pfam; PF00565; SNase; 1.
CC ProDom; PD002274; SNase; 1.
CC SMART; SM00318; SNC; 1.
CC PROSITE; PS01123; TNASE_1; FALSE_NEG.
CC PROSITE; PS01284; TNASE_2; 1.
CC PROSITE; PS00828; TNASE_3; 1.
CC KW Hypothetical protein; Hydrolase; Nuclease; Endonuclease.
FT ACT_SITE 228 228 BY SIMILARITY.
FT ACT_SITE 236 236 BY SIMILARITY.
FT ACT_SITE 270 270 BY SIMILARITY.
FT SEQUENCE 338 AA; 38073 MW; 8ADIE39F2CD32507 CRC64;

Query Match 40.6%; Score 41; DB 1; Length 338;
Best Local Similarity 53.3%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 MGNILRLFGSMTP 17
DB 1 MGNALRFLYGHCKP 15

RESULT 13
Y38K_CORSE STANDARD; PRT; 444 AA.
AC Q31852;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PERMEASE IN OSHA-CTPA INTERGENIC REGION.
GN YOJA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Park S.-H., Shin B.-S., Choi S.-K., Ghim S.-Y.;
RT "DNA sequences of a 15.4 kb fragment covering the 181 degree region of
RL the Bacillus subtilis genome.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE GNTF FAMILY OF PERMEASES.
CC
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CC
CC EMBL; AF026147; AAC17849.1; -.
CC EMBL; Z99114; CAB13843.1; -.
CC Subtilist; BG13554; yoja.
CC InterPro; IPR003474; GntP_permease.
DR
```

DR Pfam: PF02447; GntP\_permease; 1.  
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.  
FT TRANSMEM 2 22 POTENTIAL.  
FT TRANSMEM 24 44 POTENTIAL.  
FT TRANSMEM 52 72 POTENTIAL.  
FT TRANSMEM 106 126 POTENTIAL.  
FT TRANSMEM 134 154 POTENTIAL.  
FT TRANSMEM 174 194 POTENTIAL.  
FT TRANSMEM 228 248 POTENTIAL.  
FT TRANSMEM 261 281 POTENTIAL.  
FT TRANSMEM 305 325 POTENTIAL.  
FT TRANSMEM 343 363 POTENTIAL.  
FT TRANSMEM 377 397 POTENTIAL.  
FT TRANSMEM 424 444 POTENTIAL.  
SQ SEQUENCE 444 AA; 46808 MW; 69AEAG8BA3F6BBFC CRC64;

Query Match 40.6%; Score 41; DB 1; Length 444;  
Best Local Similarity 44.4%; Pred. No. 24;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 1 WLMGNILRLFGSMTPA 18  
I : :||| || I I  
Db 347 WTIAAVLRCLGSATVAA 364

## RESULT 14

GNTP\_BACLI STANDARD; PRT; 448 AA.  
AC P46832;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE GLUCONATE PERMEASE.  
GN GNTP.  
OS Bacillus licheniformis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1402;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BGSC5A2;  
RX MEDLINE-96051988; PubMed-8535972;  
RA Yoshida K.I., Seki S., Fujita Y.;  
RT "Nucleotide sequence and features of the Bacillus licheniformis gnt  
Operon.";  
RL DNA Res. 1:157-162(1994).  
CC -1- PATHWAY: GLUCONATE UTILIZATION.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE GNTP FAMILY OF PERMEASES.

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CC -----

DR EMBL; D31631; BAA06503.1; -  
DR PIR; JC2305; JC2305.  
DR InterPro; IPR003474; GntP\_permease.  
DR Pfam; PF02447; GntP\_permease; 1.  
KW Glucenate utilization; Sugar transport; Transmembrane.  
FT TRANSMEM 2 22 POTENTIAL.  
FT TRANSMEM 23 43 POTENTIAL.  
FT TRANSMEM 52 72 POTENTIAL.  
FT TRANSMEM 106 126 POTENTIAL.  
FT TRANSMEM 134 154 POTENTIAL.  
FT TRANSMEM 174 194 POTENTIAL.  
FT TRANSMEM 228 248 POTENTIAL.  
FT TRANSMEM 269 289 POTENTIAL.  
FT TRANSMEM 302 322 POTENTIAL.

FT TRANSMEM 347 367 POTENTIAL.  
FT TRANSMEM 373 393 POTENTIAL.  
FT TRANSMEM 428 448 POTENTIAL.  
SQ SEQUENCE 448 AA; 46725 MW; A8104496A124D73A CRC64;

Query Match 40.6%; Score 41; DB 1; Length 448;  
Best Local Similarity 44.4%; Pred. No. 24;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 1 WLMGNILRLFGSMTPA 18  
I : :||| || I I  
Db 351 WVIAAILRLISLGSATVAA 368

## RESULT 15

ANX6\_BOVIN STANDARD; PRT; 618 AA.  
AC P79134;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ANNEXIN VI (LIPOCORTIN VI) (P68) (P70) (PROTEIN III) (CHROMOBINDIN 20)  
DE (67 KDA CALECTRIN) (CALPHOBINDIN-II) (CPB-II) (FRAGMENT).  
GN ANX6 OR ANX6.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Camera C., Creutz C.E.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE-98422308; PubMed-9748523;  
RA Avila-Sakar A.J., Creutz C.E., Kretsinger R.H.;  
RL "Crystal structure of bovine annexin VI in a calcium-bound state.";  
RL Biochim. Biophys. Acta 1387:103-116(1998).  
CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF  
CC CA(2+) FROM INTRACELLULAR STORES.  
CC -1- DOMAIN: CONTAINS EIGHT HOMOLOGOUS REPEATS WITH A CONSENSUS  
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS  
CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.  
CC -1- PTM: PHOSPHORYLATED IN RESPONSE TO GROWTH FACTOR STIMULATION (BY  
CC SIMILARITY).  
CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.

CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.  
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CC -----

DR EMBL; U87539; AAB47570.1; -  
DR PDB; 1AVC; 28-JAN-98.  
DR InterPro; IPR001464; Annexin.  
DR Pfam; PF00191; annexin; 7.  
DR SMART; SM00335; ANX; 8.  
DR PROSITE; PS00223; ANNEXIN; 6.  
KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;  
3D-structure. 1 1  
FT NON\_TER <1 34 ANNEXIN 1.  
FT REPEAT 46 106 ANNEXIN 2.  
FT REPEAT 130 190 ANNEXIN 3.  
FT REPEAT 205 265 ANNEXIN 4.  
FT REPEAT 317 377 ANNEXIN 5.

FT REPEAT 389 449 ANNEXIN 6.  
 FT REPEAT 478 538 ANNEXIN 7.  
 FT REPEAT 553 613 ANNEXIN 8.  
 SQ SEQUENCE 618 AA; 69796 MW; 5571F70F24B5836F CRC64;

Query Match 40.6%; Score 41; DB 1; Length 618;  
 Best Local Similarity 44.4%; Pred. No. 33;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LMGNIILRLIFGSMTPAN 19  
 Db 366 LSGDLARLILGLMPPAH 383

Search completed: March 9, 2002, 00:47:36  
 Job time: 797 sec





GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:51 ; Search time 94.88 Seconds  
(without alignments)  
29.291 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101  
Sequence: 1 WLMGNILRLFLGSMWTPAN 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_17.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	68	67.3	346	11	Q9DB74	Q9db74 mus musculus
2	46	45.5	410	2	Q9KAU8	Q9kau8 bacillus ha
3	45	44.6	417	2	Q9KQ33	Q9kq33 vibrio chol
4	44	43.6	122	5	Q21462	Q21462 caenorhabdi
5	44	43.6	473	5	Q9W1Y9	Q9w1y9 drosophila
6	44	43.6	1040	5	Q9VH04	Q9vh04 drosophila
7	43.5	43.1	301	2	Q9K367	Q9k367 bacillus ce
8	43	42.6	111	6	Q9N0J0	Q9n0j0 bos taurus
9	43	42.6	175	2	Q9ET95	Q9et95 synechococc
10	43	42.6	220	8	Q9B4F4	Q9b4f4 charina bot
11	43	42.6	353	8	Q9TE66	Q9te66 skeletonema
12	43	42.6	353	8	Q9TE64	Q9te64 thalassiosi
13	43	42.6	422	2	P72725	P72725 synechocyst
14	43	42.6	691	2	Q9XDB3	Q9xdb3 staphylococ
15	43	42.6	591	2	Q9STU2	Q9stu2 staphylococ
16	43	42.6	715	5	Q9T728	Q9t728 trypanosoma
17	43	42.6	836	2	Q9KRL1	Q9krl1 vibrio chol
18	43	42.6	1016	4	Q9NXV1	Q9nxv1 homo sapien
19	42.5	42.1	403	2	Q9RT29	Q9rt29 deinococcus

20	42	41.6	422	2	Q914K4	Q914k4 pseudomonas
21	42	41.6	452	2	Q99RD0	Q99rd0 staphylococ
22	42	41.6	476	10	Q39134	Q39134 arabidopsis
23	42	41.6	605	8	Q9MEV0	Q9mev0 sciurus vul
24	41.5	41.1	215	13	P70051	P70051 xenopus lae
25	41	40.6	107	4	O43600	O43600 homo sapien
26	41	40.6	147	10	Q9LN60	Q9ln60 arabidopsis
27	41	40.6	266	2	Q9KEW5	Q9kew5 bacillus ha
28	41	40.6	513	3	Q9C1X4	Q9c1x4 schizosacch
29	41	40.6	1817	5	Q19931	Q19931 caenorhabdi
30	40.5	40.1	159	2	Q9R2K2	Q9r2k2 uncultured
31	40.5	40.1	235	5	O44109	O44109 drosophila
32	40.5	40.1	235	5	O44110	O44110 drosophila
33	40.5	40.1	247	5	O76996	O76996 drosophila
34	40.5	40.1	247	5	O77458	O77458 drosophila
35	40.5	40.1	247	5	O76995	O76995 drosophila
36	40.5	40.1	247	5	Q9TY56	Q9ty56 drosophila
37	40	39.6	123	1	Q9YDA5	Q9yda5 aeropyrum p
38	40	39.6	130	12	O55675	O55675 newcastle d
39	40	39.6	224	4	Q9NRV1	Q9nrv1 homo sapien
40	40	39.6	233	5	Q9XUQ2	Q9xuq2 caenorhabdi
41	40	39.6	255	10	O04158	O04158 arabidopsis
42	40	39.6	256	4	Q9PIR6	Q9pir6 homo sapien
43	40	39.6	256	5	Q9XUQ3	Q9xuq3 caenorhabdi
44	40	39.6	257	10	O64379	O64379 arabidopsis
45	40	39.6	264	11	Q9EST4	Q9est4 mus musculu

## ALIGNMENTS

RESULT 1

ID Q9DB74 PRELIMINARY; .PRT; 346 AA.  
AC Q9DB74;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DE PHOSPHOLIPASE A2 GROUP VII (PLATELET-ACTIVATING FACTOR  
DE ACETYLHYDROLASE, PLASMA).  
CN PLA2G7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RX [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=CEREBELLUM;  
RC MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.  
FT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK005158; BAB23849.1;  
DR MGD; MGI:1351327; Pla2g7.  
DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
DR InterPro; IPR000734; Lipase.

DR PROSITE; PS00120; LIPASE\_SER; UNKNOWN.1.  
SO SEQUENCE 346 AA; 38967 MW; D68A2A128402E554 CRC64;

Query Match 67.3%; Score 68; DB 11; Length 346;  
Best Local Similarity 66.7%; Pred. No. 0.0027;  
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMGNILRLIFGSMTPAN 19  
Db 115 IVGNILHLVGSULTTAS 132

RESULT 2  
Q9KAU8 PRELIMINARY; PRT; 410 AA.  
AC Q9KAU8;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE SPORE GERMINATION PROTEIN 1.  
GN GERAA OR BH2188.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125/JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans" and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL; AF001514; BAB05907.1; -;  
KW Complete proteome.  
SQ SEQUENCE 410 AA; 46029 MW; 20E5722AB95AB46D CRC64;

Query Match 45.5%; Score 46; DB 2; Length 410;  
Best Local Similarity 47.8%; Pred. No. 15;  
Matches 11; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 WLMGNILRL-----FGSMTP 17  
Db 213 WLMGSALRLRLITSPFIFGVLP 235

RESULT 3  
Q9KQ33 PRELIMINARY; PRT; 417 AA.  
AC Q9KQ33;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE URACIL PERMEASE.  
GN VC2171.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson S.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
RT cholerae";  
RL Nature 406:477-483(2000).  
DR EMBL; AE004288; AAF95316.1; -;  
DR TIGR; VC2171; -;  
DR InterPro; IPR000444; Xan\_ur\_permease.  
DR Pfam; PF00860; xan\_ur\_permease; 1.  
DR PROSITE; PS01116; XANTH\_URACIL\_PERMEASE; 1.  
KW Complete proteome.  
SQ SEQUENCE 417 AA; 43282 MW; 743A369DC814B7B9 CRC64;

Query Match 44.6%; Score 45; DB 2; Length 417;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMGNILRLIFGSMTT 16  
Db 323 VMGGIMILFSGSTAT 337

RESULT 4  
Q21462 PRELIMINARY; PRT; 122 AA.  
AC Q21462;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE COSMID M02D8.  
GN M02D8.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton A., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., R.,  
RA Parsons J., Percy C., Rifen L., Koopra A., Saunders D., Showkneen R.,  
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Miller N.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U41034; AAA82380.1; -;  
SQ SEQUENCE 122 AA; 13773 MW; 29ACC97CE1016D98 CRC64;

Query Match 43.6%; Score 44; DB 5; Length 122;  
Best Local Similarity 44.4%; Pred. No. 9.5;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WLMGNILRLIFGSMTPA 18  
Db 73 WVDGDIIRLVFNNSPTGA 90

RESULT 5  
Q9W1Y9

RESULT	6
O9VH04	
ID	O9VH04 PRELIMINARY; PRT; 1040 AA.
AC	O9VH04;
DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE	CGL1871 PROTEIN.
GN	CGL1871.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RC	SEQUENCE FROM N.A.
RP	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celisnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Man K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA	Arif J.F., Agbayani A., An H.-J., Andrews-Franknoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berhan B.P., Bhargava D., Boltshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., MCPerson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moyle M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paciej J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Sidgen-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA	Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng H.O.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT	"The genome sequence of Drosophila melanogaster.";
DR	Science 287:2185-2195(2000).
RL	EMBL; AE003686; AAF54517.1 -
SQ	FLYBase; FBgn0037805; CG11871.
SR	SEQUENCE 1040 AA: 1121252 MW: E63B68169E1C4896 CRC64

Query Match	43.68;	Score 44;	DB 5;	Length 1040;
Best Local Similarity	56.29;	Pred. No. 85;		
Matches	9;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

	Matches	9;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
QY	3	MCNILLRLFGSWTTTPA	18							
		: :	:	:	:	:	:	:	:	:
Db	95	VGDICOLLGTTTPA	110							

7  
PAGE 5

PROPERTY OF

ID 09K36

PRELIMINARY: PRT: 301 AA

PRELIMINARY: PRT: 301 AA

Q9K367; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE YNDD PROTEIN (PUTATIVE SPORE GERMINATION PROTEIN) (FRAGMENT).  
 YNDD.  
 GN Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 14579;  
 RA Oktstad O.A., Agasse H., Lereclus D., Kolsto A.B.;  
 RT \*20 kb DNA sequence surrounding the hbla hemolytic enterotoxin locus  
 from Bacillus cereus ATCC 14579.\*;  
 RL submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 14579;  
 RX MEDLINE=20055637; PubMed=10589720;  
 RA Oktstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;  
 RT "Sequence analysis of three Bacillus cereus loci under PicR-regulated  
 genes encoding degradative enzymes and enterotoxin.\*;  
 RL Microbiology 145:3129-3138(1999).  
 DR EMBL; AJ007795; CAB96936.1; -;  
 DR EMBL; AJ237785; CAB69787.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 301 AA; 33612 MW; 37608BDA96E03D2 CRC64;

Query Match 43.1%; Score 43.5; DB 2; Length 301;  
 Best Local Similarity 47.8%; Pred. No. 29;  
 Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 1;  
 QY 1 WLMGNILRL-----FGSWTPA 18  
 DB 93 WLPGLTLLRLRLFTAFVSLFAPA 115

RESULT 8  
 Q9N0J0 ID Q9N0J0 PRELIMINARY; PRT; 111 AA.  
 AC Q9N0J0; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE ANGIOTENSIN RECEPTOR 2 (FRAGMENT).  
 GN AT2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RA Berisha B.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=20039923; PubMed=10569984;  
 RA Acosta T., Berisha B., Ozawa T., Sato K., Schams D., Miyamoto A.;  
 RT "Evidence for local endothelin-angiotensin atrial natriuretic peptide  
 system in bovine mature follicles in vitro: effects on steroid  
 hormones and prostaglandin secretion.\*;  
 RL Biol. Reprod. 61:1419-1425(1999).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AJ277986; CAB92128.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA; 13102 MW; 9E8A81D3D580A601 CRC64;

Query Match 42.6%; Score 43; DB 6; Length 111;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WLMGNILRLFLFGSMWT 16  
 DB 17 WLFQPMVKLFGSLPT 32

RESULT 9  
 Q9ET95 ID Q9ET95 PRELIMINARY; PRT; 175 AA.  
 AC Q9ET95; 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CYTOCHROME C550 LIKE PROTEIN.  
 GN PSBV2.  
 OS Synechococcus vulcanus, and  
 OS Thermosynechococcus elongatus.  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=32053; 146786;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S. vulcanus, and T. elongatus;  
 RA Katoh H., Itoh S., Shen J., Ikeuchi M.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S. vulcanus, and T. elongatus;  
 RA Katoh H., Itoh S., Shen J., Ikeuchi M.;  
 RL "CLONING OF THE GENES FOR CYTOCHROME C550 AND A C550-LIKE PROTEIN FROM  
 THE THERMOPHILIC CYANOBACTERIUM Synechococcus elongatus.\*;  
 RL Plant Cell Physiol. 40:89-89(1999).  
 DR EMBL; AB052598; BAB20064.1; -;  
 DR EMBL; AB052597; BAB20060.1; -;  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR003218; CytC\_c550.  
 DR PRODOM; PDD00841; Cyt\_c550; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 SQ SEQUENCE 175 AA; 19118 MW; FB95EE3348651C44 CRC54;

Query Match 42.6%; Score 43; DB 2; Length 175;  
 Best Local Similarity 50.0%; Pred. No. 20;  
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 WLMGNILRLFLFGSMWTPA 18  
 DB 13 WLCGLLILLGLWTIAPA 30

RESULT 10  
 Q9B4F4 ID Q9B4F4 PRELIMINARY; PRT; 220 AA.  
 AC Q9B4F4; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE NADH DEHYDROGENASE SUBUNIT 4 (FRAGMENT).  
 OS Charina botata.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Boidae; Boidae;

OC Charina.  
OX NCBI\_TaxID=51858;  
RN [1]  
RN SEQUENCE FROM N.A.

RX MEDLINE=21097362; PubMed=11161758;  
RA Rodriguez-Robles J.A., Stewart G.R., Papenfuss T.J.;  
RT "Mitochondrial DNA-Based Phylogeography of North American Rubber Boas,  
RT Charina botatae (Serpentes: Boidae).";  
RL Mol. Phylogenet. Evol. 18:227-237(2001).  
DR EMBL: AF302976; AAK19214.1; -;  
KW Mitochondrion.  
FT NON\_TER 1  
FT SEQUENCE 220 AA; 2488 MW; 46B28E57993399A5 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 220;  
Best Local Similarity 54.5%; Pred. No. 26;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 WLMGNILRLFLF 11  
Db 125 WLMGNILMNIAT 135  
|||||: :|

RESULT 11

Q9TE66  
ID Q9TE66 PRELIMINARY; PRT; 353 AA.  
AC Q9TE66;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).  
GN COXI.  
OS Skeletonema costatum.  
OC Mitochondrion.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Thalassiosirophyceae; Thalassiosirales; Skeletonemataceae;  
OC Skeletonema.  
OX NCBI\_TaxID=2843;  
OX [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CCAP 1077-1B;  
RA Ehara M., Inagaki Y., Watanabe K.I., Ohama T.;  
RT "Phylogenetic analysis of diatom coxi genes and implications of  
RT fluctuating GC content on mitochondrial genetic code evolution.";  
RL Curr. Genet. 0:0-0(1999).  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE  
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN  
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2  
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3  
CC AND COPPER B (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) - 2 H(2)O + 4  
CC FERROCYTOCHROME C.  
CC -!- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).  
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL: AB020227; BAA86612.1; -;  
DR InterPro: IPR000883; COXI.  
DR PRINTS: PF00115; COXI; 1.  
DR PROSITE: PS00077; COXI; 1.  
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;  
FT Respiratory chain; Transmembrane.  
FT NON\_TER 1  
FT SEQUENCE 353 AA; 38158 MW; F107054A59A65521 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 353;  
Best Local Similarity 55.6%; Pred. No. 41;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 WLMGNILRLFLFGSWTPA 18  
Db 90 WLLPFSLLLLFASMLTEA 107  
||: | || | | | |

RESULT 12

Q9TE64  
ID Q9TE64 PRELIMINARY; PRT; 353 AA.  
AC Q9TE64;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).  
GN COXI OR COX1.  
OS Thalassiosira nordenskioldii.  
OC Mitochondrion.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Thalassiosirophyceae; Thalassiosirales; Thalassiosiraceae;  
OC Thalassiosira.  
OX NCBI\_TaxID=83372;  
OX [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CCMP992;  
RA Ehara M., Inagaki Y., Watanabe K.I., Ohama T.;  
RT "Phylogenetic analysis of diatom coxi genes and implications of  
RT fluctuating GC content on mitochondrial genetic code evolution.";  
RL Curr. Genet. 0:0-0(1999).  
CC [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CCMP992;  
RA Ehara M., Watanabe K.I., Hiraiwa N., Ohama T.;  
RT "Distribution of the cognate group II trops detected in the  
RT mitochondrial gene of a diatom and a haptophyte.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE  
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN  
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2  
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3  
CC AND COPPER B (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) - 2 H(2)O + 4  
CC FERROCYTOCHROME C.  
CC -!- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).  
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL: AB020229; BAA86614.1; -;  
DR EMBL: AB038235; BAA86616.1; -;  
DR InterPro: IPR000883; COX1.  
DR Pfam: PF00115; COXI; 1.  
DR PRINTS: PR01165; CYCOXIDASE1.  
DR PROSITE: PS00077; COXI; 1.  
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;  
FT Respiratory chain; Transmembrane.  
FT NON\_TER 1  
FT SEQUENCE 353 AA; 38158 MW; F107054A59A65521 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 353;  
Best Local Similarity 55.6%; Pred. No. 41;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 WLMGNILRLFLFGSWTPA 18  
Db 90 WLLPFSLLLLFASMLTEA 107  
||: | || | | | |

RESULT 13  
P72725

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ID P2725 PRELIMINARY; PRT; 422 AA.
AC P2725;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HYPOTHETICAL 45.7 KDA PROTEIN.
GN SLR1411.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyaajima N., Hirosewa M., Sugliura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90900; BAA16733.1; -.
DR InterPro: IPR002822; DUF111.
DR Pfam: PF01969; DUF111; 1.
DR ProDom: PD018127; DUF111; 1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 422 AA; 45731 MW; 38161945A217A492 CRC64;

Query Match 42.6%; Score 43; DB 2; Length 422;
Best Local Similarity 52.9%; Pred. No. 50;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 MGNILRLFGSMWTPAN 19
DB 238 LANILRLWIGTEITPHN 254

RESULT 14
Q9XDB3 PRELIMINARY; PRT; 691 AA.
AC Q9XDB3;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PENICILLIN-BINDING PROTEIN PBP2B (PENICILLIN-BINDING PROTEIN 3).
GN PBP2B OR PBP3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ISP3;
RA Komatsuzawa H., Choi G.H., Ohta K., Sugai M., Tran M.T., Suganaka H.;
RT "Cloning and characterization of a gene, pbpF, encoding a new
RT penicillin-binding protein, PBP2B, in Staphylococcus aureus.";
RL Antimicrob. Agents Chemother. 43:1578-1583(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=COL;
RC MEDLINE=20115552; PubMed=10648534;
RA Pinho M.G., Lencastre H., Tomasz A.;
RT "Cloning, Characterization, and Inactivation of the Gene pbpC,
RT Encoding Penicillin-Binding Protein 3 of Staphylococcus aureus.";
RL J. Bacteriol. 182:1074-1079(2000).
DR EMBL: AF098801; AAD43176.1; -.
DR EMBL: AJ243120; CAB72261.1; -.
DR InterPro: IPR001460; Transpeptidase.
DR Pfam: PF00905; Transpeptidase; 1.
SQ SEQUENCE 691 AA; 77238 MW; 4D9D2EA0DCCCE3691 CRC64;
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Query Match 42.6%; Score 43; DB 2; Length 691;  
Best Local Similarity 53.3%; Pred. No. 83;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILRLFGSMWTPA 18  
DB 235 GDTLRGIFGDVSTPA 249

RESULT 15  
Q99TU2

ID Q99TU2 PRELIMINARY; PRT; 691 AA.  
AC Q99TU2;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE PENICILLIN-BINDING PROTEIN 3.

GN PBP3 OR SAI381.

OS Staphylococcus aureus subsp. aureus N315.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Staphylococcus.

OX NCBI\_TaxID=158879;

RN [1]

RP SEQUENCE FROM N.A.

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

RA Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus.";

RL Lancet 357:1225-1240(2001).

DR EMBL: AF003134; BAB42644.1; -.

KW Complete proteome.

SQ SEQUENCE 691 AA; 77234 MW; 4D9FESA0DCCFED91 CRC64;

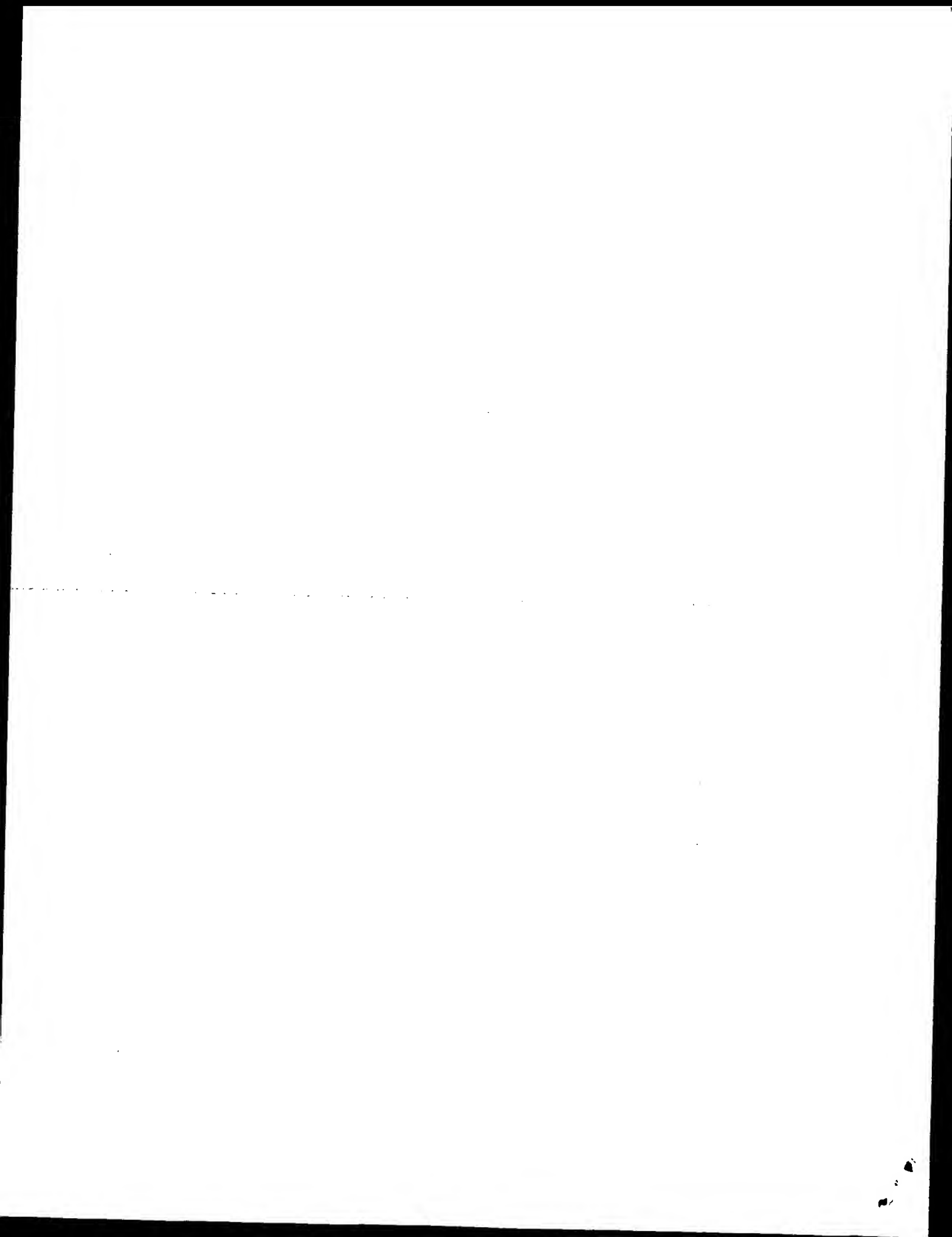
Query Match 42.6%; Score 43; DB 2; Length 691;  
Best Local Similarity 53.3%; Pred. No. 83;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILRLFGSMWTPA 18  
DB 235 GDTLRGIFGDVSTPA 249

Search completed: March 9, 2002, 00:46:53  
Job time: 829 sec

us-09-922-067-4.rspt

Mon Mar 11 10:02:11 2002





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 20:38:16 ; Search time 1981.93 Seconds  
(without alignments)  
11328.685 Million cell updates/sec

Title: US-09-922-067-9  
Perfect score: 1361  
Sequence: 1 TCAGAGACTAAGCTGAAACT.....AGGAATAGAGAAATACAATT 1361

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_lm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_lm.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htgo\_hum.\*
- 31: em\_htgo\_inv.\*
- 32: em\_htgo\_rod.\*
- 33: em\_htg\_hum.\*
- 34: em\_htg\_inv.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

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2	1361	100.0	1361	6	AR080658	AR080658 Sequence
3	1361	100.0	1361	6	AR084987	AR084987 Sequence
4	1361	100.0	1361	6	ARI25358	ARI25358 Sequence
5	1361	100.0	1361	6	AX006795	AX006795 Sequence
6	1361	100.0	1361	9	HSU24577	U24577 Human LDL-p
7	1359.4	99.9	1359	6	HSU20157	U20157 Human plate
8	1359.4	99.9	1359	6	AR1377	AR1377 Sequence 7
9	1359.4	99.9	1359	6	AR064404	AR064404 Sequence
10	1359.4	99.9	1359	6	AR083755	AR083755 Sequence
11	1359.4	99.9	1359	6	ARI41150	ARI41150 Sequence
12	1359.4	99.9	1359	6	ARI42503	ARI42503 Sequence
13	1359.4	99.9	1359	6	I23385	I23385 Sequence 7
14	1359.4	99.9	1359	6	I49901	I49901 Sequence 7
15	1359.4	99.9	1359	6	I60362	I60362 Sequence 7
16	1359.4	99.9	1359	6	I85595	I85595 Sequence 7
17	1362.4	85.4	1335	6	AR1400	AR1400 Sequence 30
18	1162.4	85.4	1335	6	AR064425	AR064425 Sequence
19	1162.4	85.4	1335	6	AR083776	AR083776 Sequence
20	1162.4	85.4	1335	6	ARI41171	ARI41171 Sequence
21	1162.4	85.4	1335	6	ARI42524	ARI42524 Sequence
22	1162.4	85.4	1335	6	I60383	I60383 Sequence 30
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24	1049.6	77.1	1533	6	AR1393	AR1393 Sequence 23
25	1049.6	77.1	1533	6	AR064419	AR064419 Sequence
26	1049.6	77.1	1533	6	AR083770	AR083770 Sequence
27	1049.6	77.1	1533	6	ARI41165	ARI41165 Sequence
28	1049.6	77.1	1533	6	ARI42518	ARI42518 Sequence
29	1049.6	77.1	1533	6	I60377	I60377 Sequence 23
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35	1043.2	76.6	2191	6	I49915	I49915 Sequence 22
36	1043.2	76.6	2191	6	I60376	I60376 Sequence 22
37	1043.2	76.6	2191	6	I85609	I85609 Sequence 22
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41	783.6	57.6	1494	6	AR1391	AR1391 Sequence 21
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ALIGNMENTS

RESULT 1

A41956  
LOCUS A41956  
DEFINITION Sequence 9 from Patent WO9500649.  
ACCESSION A41956  
VERSION A41956.1 GI:2297493  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1361)  
AUTHORS Macphree,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S., Lawrence,G.M. and Rice,S.O.  
TITLE LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 27, INHIBITORS THEREOF AND USE OF THE SAME IN DIAGNOSIS AND THERAPY  
JOURNAL Patent: WO 9500649-A 9 05-JAN-1995;  
COMMENT SMITHKLINE BEECHAM PLC (GB)  
Other publication JP 8500740T 960130.  
FEATURES  
source 1. .1361

PAT 05-MAR-1997

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Db	1321	CATCATGTTTACAGAACCTCTTCAGGAATACAGAAATYACAANT	1361			
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AR080658						
LOCUS	AR080658	1361 bp	DNA			
DEFINITION	Sequence 9 from patent US 5968818.					
ACCESSION	AR080658					
VERSION	AR080658.1					
KEYWORDS	GI:10007388					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1361)					
TITLE	Glover R.I., Simon, Lawrence, G., MarkProuse and Rice, S. QuentynJohn.					
JOURNAL	Lipoprotein associated phospholipase A2, inhibitors thereof and					
FEATURES	of the same in diagnosis and therapy					
source	Patent: US 5968818-A 9 19-OCT-1999;					
	Location/Qualifiers					
	1..1361					
	/organism="unknown"					
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ORIGIN	393 t					
Query Match						
Best Local Similarity 100.0%; Score 1361; DB 6; Length 1361;						
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps						
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RESULT	2
AR080658	
LOCUS	1361 bp DNA
DEFINITION	Sequence 9 from patent US 5968818.
ACCESSION	AR080658
VERSION	AR080658.1 GI:10007388
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1361)
TITLE	Gloger I., Simon, Lawrence, G. Mark Prouse and Rice, S. Quentyn John. Lipoprotein associated phospholipase A2, inhibitors thereof and of the same in diagnosis and therapy
JOURNAL	Patent: US 5968818-A 9 19-OCT-1999;

Qy 61 GCTTTTCTGCTCTGGGCTGCTGGCTGCTGGTTATCTCTTTGACTGGCAATACATAA 120  
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Qy 241 AGACTTAATGTTTGATCACAATAAAGGACACCTCTCTGCGTTTATATCCATCCCA 300  
Db 241 AGACTTAATGTTTGATCACAATAAAGGACACCTCTCTGCGTTTATATCCATCCCA 300  
Qy 301 AGATAATGATCGCTTGACACCTCTTGATCCCAATAAAGAAATATTTTGGGCTCTAG 360  
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Qy 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTCAAT 420  
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Qy 421 GACAACTCTCGAACTGAATTCCTCTGAGGCTGGTGAAGAAATATCACTTGTGT 480  
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Qy 901 ATTCAGATGTTGTTATGCTGATGATGTTTCCACTGGGTGATGAAGTATATTC 960  
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Qy 961 CAGAAATCTCAGCCCTCTTTTATCAACCTCTGAATATTTCCAAATATCCTGTAATAT 1020  
Db 961 CAGAAATCTCAGCCCTCTTTTATCAACCTCTGAATATTTCCAAATATCCTGTAATAT 1020  
Qy 1021 CATTAATAATGAAAAATGCTACTCAGCTGATAAAGAAAGAGATGATTACAACTCAGGG 1080  
Db 1021 CATTAATAATGAAAAATGCTACTCAGCTGATAAAGAAAGAGATGATTACAACTCAGGG 1080  
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RESULT 3  
AR084987  
LOCUS AR084987 1361 bp DNA PAT 01-SEP-2000  
DEFINITION Sequence 9 from patent US 5981252.  
ACCESSION AR084987  
VERSION AR084987.1 GI:10011758  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1361)  
AUTHORS MacPhee,C.Houston and Tew,D.Graham.  
TITLE Lipoprotein associated phospholipase A.sub.2, inhibitors thereof  
and use of the same in diagnosis and therapy  
JOURNAL Patent: US 5981252-A 9 09-NOV-1999;  
FEATURES  
LOCATION/Qualifiers  
source 1. 1361  
BASE COUNT 417 a 273 c 278 g 393 t  
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Query Match 100.0%; Score 1361; DB 6; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 181 TCGAAGCTTTGGCCAACTAATAAATCCCGGGGAATGGCCCTTATTCCTGTTTATATCCATCCCA 240  
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Qy 241 AGACTTAATGTTTGATCACAATAAAGGACACCTCTCTGCGTTTATATCCATCCCA 300  
Db 241 AGACTTAATGTTTGATCACAATAAAGGACACCTCTCTGCGTTTATATCCATCCCA 300  
Qy 301 AGATAATGATCGCTTGACACCTTTTGATCCCAATAAAGAAATATTTTGGGCTCTTAG 360  
Db 301 AGATAATGATCGCTTGACACCTTTTGATCCCAATAAAGAAATATTTTGGGCTCTTAG 360  
Qy 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTCTTTGGTCAAT 420  
Db 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTCTTTGGTCAAT 420  
Qy 421 GACAACTCTCGAACTGAATTCCTCTGAGGCTGGTGAAGAAATATCACTTGTGT 480  
Db 421 GACAACTCTCGAACTGAATTCCTCTGAGGCTGGTGAAGAAATATCACTTGTGT 480

Qy	481	TTTTTCTCATGGTCTTGGGCACTTCAGGACACTTTATCTGCTATTGGCAATTGACCTGGC	540
Db	481	TTTTTCTCATGGTCTTGGGCACTTCAGGACACTTTATCTGCTATTGGCAATTGACCTGGC	540
Qy	541	ATCTCATGGGTTTTATAGTTGCTGCTGTAGAACACAGAGATNGATCTGCAATCTTGAACCTTA	600
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Qy	841	AGTAATTGGACATCTCTTTTGGTGGAGCAACGGTTATTCAGACTCTTACTGAAGATCAGAG	900
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Qy	901	ATTCAAGATGTGGTATTGCCCTGGATGCAATGATGTTCCACTGGTGATGAAGTATATTC	960
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Qy	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCGACTATTCGATTCAGCAAAAGCTTC	1200
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Qy	1201	ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGCATCAGTGGGACTGCTT	1260
Db	1201	ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGCATCAGTGGGACTGCTT	1260
Qy	1261	GATTGAAGGAGATGATGAGAACTTTATTTCCAGGGCCACCAATTAACACACCAATCAACA	1320
Db	1261	GATTGAAGGAGATGATGAGAACTTTATTTCCAGGGCCACCAATTAACACACCAATCAACA	1320
Qy	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT	1361
Db	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT	1361

## RESULTS

	PAT	16-MAY-2001
RESULTS <sup>4</sup>		
AR125358	AR125358	1361 bp DNA
LOCUS	Sequence 9 from patent US 6177357.	
DEFINITION		
ACCESSION	AR125358	
VERSION	AR125358.1	GI:14111420
KEYWORDS	. . .	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified. 1 (bases 1 to 1361)	

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 Qy 901 ATTGAGATGGGTATTTGCCCTGGATGATGATGATTTCCACTGGGTGATGAAGTATATTC 960  
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 Qy 1021 CATAAAAATGAAAAATGCTACTACCTCGATTAAGAAAGAAAGATGATTAACAATCAGGG 1080  
 Db 1021 CATAAAAATGAAAAATGCTACTACCTCGATTAAGAAAGAAAGATGATTAACAATCAGGG 1080  
 Qy 1081 TTAGTCCACAGAAATTTTCTGACTTTCACCTTTTGCACCTGCAAAATTAATTTGACACAT 1140  
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 DEFINITION Sequence 9 from Patent EP0974663.  
 ACCESSION AX006795  
 VERSION AX006795.1 GI:9994827  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1361)  
 Gloger, I.S., Hickey, D.M., Macpherson, C.H., Southan, C.D.,  
 Lawrence, G.M., Rice, S.Q. and few.D.G.  
 Lipoprotein associated phospholipase a2, inhibitors thereof and use  
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 Patent: EP 0974663-A 9 26-JAN-2000;  
 SMITHKLINE BEECHAM PLC (GB)  
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 ACCESSION U24577  
 VERSION U24577.1 GI:1314245

KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1561)  
 AUTHORS Tew D.G., Southern, C., Rice, S.O., Lawrence, M.P., Li, H., Boyd, H.F., Moores, K., Glover, I.S. and Macphree, C.H.  
 TITLE Purification, properties, sequencing, and cloning of a lipoprotein-associated, serine-dependent phospholipase involved in the oxidative modification of low-density lipoproteins  
 JOURNAL Arterioscler. Thromb. Vasc. Biol. 16 (4), 591-599 (1996)

MEDLINE 96197208  
 REFERENCE 2 (bases 1 to 1561)  
 AUTHORS Rice, S.O.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-APR-1995) Simon O.J. Rice, Smithkline Beecham Pharmaceuticals, New Frontiers Science Park North, Third Avenue, Harlow, Essex CM195AW, UK  
 COMMENT On May 16, 1996 this sequence version replaced gi:790655.

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RESULT 7

HSU20157 1505 bp mRNA PRI 21-APR-1995  
 LOCUS Human platelet-activating factor acetylhydrolase mRNA, complete cds  
 DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Tjoelker, L.W., Wilder, C., Eberhardt, C., Stafforini, D.M., Diesch, G., Schimpf, B., Hooper, S., Trong, H., Cousins, L.S., Zimmerman, G.A., Yamada, Y., McIntyre, T.M., Prescott, S.M., and Gray, P.W.  
 Anti-inflammatory properties of a platelet-activating factor acetylhydrolase  
 Nature 374 (6522), 549-553 (1995)  
 95214779  
 2 (bases 1 to 1505)  
 Tjoelker, L.W.  
 Direct Submission  
 Submitted (20-JAN-1995) Larry W. Tjoelker, ICOS Corporation, 22021 20th Ave. S.E., Bothell, WA 98021, USA  
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REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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DEFINITION Sequence 7 from Patent WO9909147.  
ACCESSION AB1377  
VERSION AB1377.1 GI:6731692  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1520)  
AUTHORS Eberhardt, C.D. and Gray, P.  
TITLE TRUNCATED PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE  
JOURNAL Patent: WO 9909147-A 7 25-FEB-1999;  
ICOS CORP (US)

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LOCUS	AR064404
DEFINITION	Sequence 7 from patent US 5847088.
ACCESSION	AR064404
VERSION	AR064404.1 GI:5993712
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1520)
AUTHORS	Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le, Tjoelker,I.W. and Wilder,C.L.
TITLE	Antibodies specific for platelet-activating factor acetylhydrolase
JOURNAL	Patent: US 5847088-A 7 08-DEC-1998;
FEATURES	Location/Qualifiers 1..1520 /organism="unknown"
BASE COUNT	453 a 311 c 333 g 423 t
ORIGIN	

Query Match	99.9%	Score 1359.4	DB 5	Length 1520	0			
Best Local Similarity	99.9%	Pred. No. 0						
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Qy	121	TCCTGTTGGCCATATGAAATCAATCAGCATGGGTCAACAAAATACAGTACTGATGGCTGC	180					
Db	245	TCCTGTTGGCCATATGAAATCAATCAGCATGGGTCAACAAAATACAGTACTGATGGCTGC	304					
Qy	181	TGCAAGCTTTTGSCCAAACTAAAATCCCCGGGGAAATGGGCCCTTATTCCGTTGGTTGTAC	240					
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Qy	241	AGACTTAATGTTTGATCACACTAATAAGGGACACTCTCTGGTTTATTTATCCATCCCA	300					
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Qy	421	GACAACTCTCGAAACTGGAATTCGCCCTCTGAGGCGTGGTAAATAATATCCACTTTGTTGT	480					
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ACCESSION	Sequence 7 from patent US 5977308.
VERSION	AR083755
KEYWORDS	AR083755.1 GI:10010526
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1520) Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le, Tjoelker,L.W. and Wilder,C.L.
TITLE	Platelet-activating factor acetylhydrolase









DEFINITION Sequence 7 from patent US 5656431.

ACCESSION 160362

VERSION 160362.1

KEYWORDS GI:2478807

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 1520)

Cousens, L.S., Eberhardt, C.D., Gray, P., Trong, H. Le, Tjoelker, L.W.

and Wilder, C.L.

TITLE Platelet-activating factor acetylhydrolase

JOURNAL Patent: US 5656431-A 7 12-AUG-1997;

FEATURES Location/Qualifiers

1..1520

Source /organism="unknown"

BASE COUNT 453 a 311 c 333 g 423 t

ORIGIN

Query Match 99.9%; Score 1359.4; DB 6; Length 1520;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 125 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGGCCACCAAAATTCATGT 184  
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QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGAGTTTACTCTTTGGTTCAAT 420  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 22:03:27 ; Search time 174.17 Seconds  
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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1359.4	99.9	1520	19	AAQ96127
7	1359.4	99.9	1520	20	AAQ08463
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15	1247.8	91.7	1320	22	AAQ04169	Mouse-human plasma
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19	1162.4	85.4	1335	21	AAQ10885	Human PAF-AH cDNA
20	1162.4	85.4	1335	21	AAQ24261	Human plasma plate
21	1162.4	85.4	1335	22	AAQ89078	Platelet-activatin
22	1049.6	77.1	1533	18	AAQ87066	Bovine platelet-ac
23	1049.6	77.1	1533	20	AAQ08478	Bovine PAF-AH codi
24	1049.6	77.1	1533	20	AAQ08552	CDNA encoding plat
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26	1049.6	77.1	1533	21	AAA10879	Bovine PAF-AH cDNA
27	1049.6	77.1	1533	21	AAZ24255	Bovine plasma plat
28	1049.6	77.1	1533	22	AAQ04158	Platelet-activatin
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34	1043.2	76.6	2191	19	AAQ96129	Canine plasma plat
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42	783.6	57.6	1494	16	AAQ87948	Mouse platelet-act
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ALIGNMENTS

RESULT 1  
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ID AAQ81780 standard; cDNA; 1361 BP.  
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AC AAQ81780;  
XX  
DT 18-AUG-1995 (first entry)  
XX  
DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.  
XX  
KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;  
KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 38..1357  
FT /\*tag= a  
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XX 24-JUN-1994; 94WO-GB01374.  
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XX  
XX Gloger IS, Hickey DMB, Lawrence GMP, Macphee CH;  
XX Rice SQJ, Southan CB, Tew DG;  
XX

WPI; 1995-052086/07.

DR P-PSDB; AAR64928.

XX Purified lipoprotein associated phospholipase A2 - used to  
 PT develop prods. for diagnosis and therapy, partic. inhibitors for  
 PT treatment of atherosclerosis

XX Claim 8; Page 19; 29pp; English.

CC This sequence encodes an enzyme which may be used in a method of  
 CC screening compounds to identify those compounds which inhibit  
 CC Lp-PLA2 which involves contacting isolated Lp-PLA2 with a test  
 CC compound and measuring the rate of turnover of an enzyme substrate  
 CC as compared with the rate of turnover in the absence of the test  
 CC compound.

SQ Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 other;

Query Match 100.0%; Score 1361; DB 16; Length 1361;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1261 gattgaaggagatgatgagaatcttattccagggaaccaacatacaacaaccaatcaaca 1320  
 Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGACATACAAATTT 1361  
 Db 1321 catcatgttacagaaactcttcagggaatagagaatacaact 1361

## RESULT 2

AA52357  
 ID AA52357 standard; cDNA; 1361 BP.

XX AA52357;

XX XX  
 DT 18-SEP-2000 (first entry)

XX cDNA encoding human low density lipoprotein-associated phospholipase A2.

XX Human; low density lipoprotein associated phospholipase A2;  
 KW LDL-PLA2; plasma PAF acetyl hydrolase; recombinant; purification;  
 KW short chain phospholipid; serine-dependent phospholipase;  
 KW inflammation; proinflammatory; anti inflammatory; drug screening;  
 KW antibody; diagnosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

PH CDS 38..1360

FT /tag= a

FT /partial

FT /product= "Human LDL-PLA2"

FT /note= "No stop codon given in the specification"

XX WO200024910-A1.

PN 04-MAY-2000.

PD 27-OCT-1999; 99WO-GB03551.

XX



AA087947;  
 06-DEC-1995 (first entry)  
 Human platelet activating factor, acetyl hydrolase (PAF-AH), cDNA.  
 Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 disease; pleurisy; diagnosis, ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 162..1487  
 /tag= a  
 /product= Acetyl\_hydrolase.  
 WO9509921-A.  
 13-APR-1995.  
 06-OCT-1994; 94WO-US11340.  
 06-OCT-1993; 93US-01133803.  
 (ICOS-) ICOS CORP.  
 Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 Wilder CL;  
 WPI: 1995-155262/20.  
 P-PSDB; AAR71913.  
 New nucleic acid encoding platelet activating factor,  
 acetyl:hydrolase - useful in diagnosis and for treating  
 inflammatory diseases, e.g. pleurisy  
 Claim 4; Page 51-53; 88pp; English.  
 The human acetyl hydrolase gene (AA087947) has been isolated and  
 purified. The platelet activating factor acetyl hydrolase (AAR71913)  
 is useful in the treatment of inflammatory diseases, in particular  
 pleurisy, asthma, rhinitis and eczema. The gene may also be used in  
 raising monoclonal antibodies specific for PAF-AH that are useful in  
 the diagnosis of such diseases.  
 Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;  
 Query Match 99.9%; Score 1359.4; DB 16; Length 1520;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCAAAATTCGATGT 60  
 DB 125 tgagagactaagctgaaactgctgctcagctcccaagatgggcccacccaattgcatgt 184  
 QY 61 GCTTTTCTCCCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 DB 185 gcttttctccctcgggctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244  
 QY 121 TCGTGTGCCCCATGAATCATCATGAGTGGGTCAACAAAATACAAATGATGCTGCTGCTGCT 180  
 DB 245 tctgtgtgcccatagaatcatcatgagctgggtcaacaaaatacaatgactgctgctgctg 304  
 QY 181 TCGAGCTTTGGCCCAACTAAATCCCGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCTGCT 240  
 DB 305 tgcagctttggcccaactaaatcccggggaaatgggcttattccctgctgctgctgctgct 364  
 QY 241 AGACTTATGTTTGTATCATCAATAAAGGACCTTCTTGGCTTTATATATATATATATATATAT 300  
 DB 365 agactaatgtttgtatcatcaataaagggaacctctctgctgtttatattatcatccacca 424  
 QY 301 AGATAATGATCGCCTTGACACCTTTGGATCCCAAAATGAAGAAATATTTTGGGCTCTTAG 360

DB 425 agataatgatcgcttgacacacctttggatcccaataaagaataatttttgggtcttag 484  
 QY 361 CAAATTTCTTGGCAACACACTGCTTTATGGGCAACATTTTGGGTTACTTCTTGGTTCAT 420  
 DB 485 caaattcttgaaacacactggcttatgggcaacattctggaggttacctttgggtccaat 544  
 QY 421 GACAACTCTGCAAACTGGAATCCCTCTCTGAGGCTGCTGAAAAATATCCACTGTGTGT 480  
 DB 545 gacaaactctgcaaaactggaattccctctgagcctgtgtaaaataatccactgttgt 604  
 QY 481 TTTTCTCATGCTTGTGGGCAATTCAGGACACTTATTTCTGCTATTTGGCATTTGACCTGGC 540  
 DB 605 ttttctcatgctcttgaggcattcaggacactttattctgctattggcattgacctggc 664  
 QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTCATCTGCAACTTA 600  
 DB 665 atctcatgggtttatagttgctgtgtagaacacagagatagatctgcatctgcaactta 724  
 QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAACAGTCTTTGGCTCTACCTTGAAC 660  
 DB 725 ctattcaaggaccaaactctgctgcagaaataggggcaagctcttggctctaccttagac 784  
 QY 661 CCTGAACAAGAGGAGGAGACACAATACGAATGAGCAGGTAGCGGCAAGAGCAAGA 720  
 DB 785 cctgaacaagagagagagacacatacacgaatgagcaggtacggcaagagcaaaaga 844  
 QY 721 AATGTTCCCAAGCTCTCAGTCTCTGATTTCTTGACATTTGATGCAATCTTTAGTCAAGATCAG 780  
 DB 845 atgtcccaagctctcagctctgattcttgacattgacatgcaatggaagccagtgaagatgc 904  
 QY 781 ATTAGATTTAAAGTTTCATATGGCAACACTGCAAGGACTCTTATTCATAGGAAAAATATTC 840  
 DB 905 attagatttaagcttgataggcaaacctggaagggactctattgagggaaaaataagc 964  
 QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTCAAGATCAGAG 900  
 DB 965 agtaattggacattcttttggtygagcaacggtatttcagactcttagtgaagctcagag 1024  
 QY 901 ATTCCAGATGTGGTATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 1025 attcagatgtggtattgctccctggatgcatgagatgcttcttccactggggtgaggaagatc 1084  
 QY 961 CAGAAATCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTCTAATAT 1020  
 DB 1085 cagaattccctcagccctctttttatcaactctgaaattttcccaataatctctgctaatat 1144  
 QY 1021 CATAAAAATGAAAAATGCTACTCAGCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1080  
 DB 1145 cataaaaatgaaaaatgctactcactcagataaagaaagaaagatgatlacaaatcagggg 1204  
 QY 1081 TCCAGTCCACACAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATTAATTTGGACAT 1140  
 DB 1205 ttcagtcacacagaaatttggctgactctacttttgcactggcaaaataatttggacacat 1264  
 QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGACGCTATTTGATCTTTAGCAACAAAGCTTC 1200  
 DB 1265 gctcaaatlaaaggaggagacatagattcaaatgtagctattgtattcttagcaacaaagcttc 1324  
 QY 1201 ATTAGCATTTTCAAAAAGCATTTAGACTTCTATAAGATTTTGTAGTCAGTGGGACTGCTT 1260  
 DB 1325 attagcatcttcaaaaagcatttagacttcaataagattttgatcagttggagctgctt 1384  
 QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACAAACCAATCAACA 1320  
 DB 1385 gattgaaggagatgagagaatcttattccagggaaccaacataaacacaaccaacaa 1444  
 QY 1321 CATCATGTTTACAGAACTCTTCAGGAATACAGAAATACAAAT 1361  
 DB 1445 catcalgttacagaacctcttccagggaatagagaaatcacatt 1485

RESULT 4



QY 1141 GCTCAATTAAGGAGACATAGATTCAATGACGCTATTGATCTTAGCAACAAGCTTTC 1200  
 Db 1265 gctcaaatbaagagacatagattcaaatgacgctattgattcttagcaacaagcttc 1324  
 QY 1201 ATTAGCATCTTACAAAAGCATTTAGGACTTTCATAAAGATTTTGATCACTGGGACTGCTT 1260  
 Db 1325 attagcattctcaaaaagcatttagacttcataaagattttgatcagtggaactgctt 1384  
 QY 1261 GATTGAGGAGATGATGAGAACTTTATTCAGGGACCAACATTTACACAAACCAATCAACA 1320  
 Db 1385 gattgagagagatgagaaactttatccaggagacacattacacaaacaaatcaaca 1444  
 QY 1321 CATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361  
 Db 1445 catcatgtttacagaactcttcaggaaatagagaaatcaactt 1485

## RESULT 5

AAT80564  
 ID AAT80564 standard; cDNA; 1520 BP.  
 AC AAT80564;  
 XX  
 DT 04-NOV-1997 (first entry)  
 XX  
 DE Human plasma platelet activating factor acetylhydrolase encoding cDNA.  
 KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;  
 KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;  
 KW central nervous system shock; arthritis; Crohn's disease;  
 KW systemic lupus erythematosus; adult respiratory distress syndrome; ss.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers

CDS 162..1487

/\*tag= a

/product= PAF-AH

US5641669-A.

24-JUN-1997.

06-OCT-1993; 93US-0133803.

06-OCT-1994; 94US-0318905.

06-OCT-1993; 93US-0133803.

(ICOS-) ICOS CORP.

Cousens LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
 Wilder CL;

WPI: 1997-340947/31.

P-PSDB: AAW23796.

New human plasma platelet activating factor acetylhydrolase -

useful as anti-inflammatory for treatment of asthma, anaphylaxis,

shock, etc

Example 3; Column 35-38; 43pp; English.

The present sequence encodes the purified and isolated human plasma

platelet activating factor acetylhydrolase (PAF-AH). This novel

polypeptide inactivates PAF and oxidatively fragmented phospholipids

such as pro-inflammatory arachidonic acid metabolites, and so can be

used to treat inflammation by augmenting endogenous activity. Typical

applications are in asthma, anaphylaxis, shock, reperfusion injury,

central nervous system shock, arthritis, Crohn's disease, systemic

lupus erythematosus, adult respiratory distress syndrome. The

polypeptide can also be used to raise specific antibodies (Ab) which

are useful as immunoassay reagents and for generating anti-idiotypic

CC antibodies. The nucleic acid (present sequence) can be used to screen  
 CC for related genes; in hybridisation assays to assess the protein-  
 CC producing cells; to generate knockout mice; to detect genetic mutations  
 CC and (antisense sequences) to inhibit the protein expression. Unlike PAF  
 CC receptor antagonists, the protein is a natural component of plasma.

XX Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 18; Length 1520;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAGCTGAACCTGCTGCTCAGCTCCCAAGCTGTCGCCACCCCAATTCGATGT 60  
 Db 125 tgagagactaagctgaaactgctgctcagctcccaagctgctgcccccaaatgcatgt 184  
 QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 185 gcttttctgctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 184  
 QY 121 TCCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAACTACTGATGGCTGC 180  
 Db 245 tccctgtgcccatatgaaatcatcagcatgggtcaacaaatacaaactactgctgctgc 304  
 QY 181 TGCAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 240  
 Db 305 tgcagctttggccaaactaaatcccggggaaatgggcttatttcctgctgctgctgctgct 364  
 QY 241 AGACTTAATGTTGATCACACTAATAGGCGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 365 agacttaattgtgatcacactaataaaggacacctctctgctgctgctgctgctgctgctgct 424  
 QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGAAATATTTTGGGCTCTTAG 360  
 Db 425 agataatgatcgcttgacacctttggatcccaataaagaatatttttgggctcttag 484  
 QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGCTTACTCTTCTGCTCAAT 420  
 Db 485 caaatcttggaaacacactggcttattgggcaacattttgaggttactcttgggttcaat 544  
 QY 421 GACAACTCTGCAAACTGGAAATCCCTCTGAGGCTCTGGTGAATAATATCCAGCTTGTGT 480  
 Db 545 gacaactctgcaaaactggaaatccctctgagggcctggtgaaaaataccactgtgt 604  
 QY 481 TTTTCTCATGGTCTTGGGCAATTCAGGACACTTATTTCTGCTATTTGGCAATTCAGCTGCG 540  
 Db 605 ttttctcatggcttggggcatttcaggaacctttatctgctatttggcattgacctgac 664  
 QY 541 ATCTCATGGGCTTATAGTTCTGCTGTAGACACAGATAGATCTGCATCTGCAACTTA 600  
 Db 565 atctcatgggcttattagttgctgctgtagaacacagagatagatctgcatctgcaactta 724  
 QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660  
 Db 725 ctatttcaaggaccaatctgctgcagaaatagggacaaagtcttggctacctcttagaac 784  
 QY 661 CTTGAACAAAGAGGAGGACACATATACGAATGACAGCTACGGCAAGAGCAACAAAGA 720  
 Db 785 cttgaacaagaggaggagacacataacgaatgagcaggtacgccaagagcaaaaga 844  
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATTTGATGAAAGCCAGTGAAGATGC 780  
 Db 845 atgttcccaagctctcagctgctgattcttgacattgatacaggaagccagtgaaagatgc 904  
 QY 781 ATTAGATTTAAAGTTTATGATGCAACTGAAGGACTCTATTGATGAGGAAATAGC 840  
 Db 905 attagatttaaagtttgaatgagaaactgaggaactctatctgagaggaagaaatagc 964  
 QY 841 AGTAATTTGACATTTCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 900  
 Db 965 agtaattgacattcttttggaggcaacggttatttcagactcttagtgaagatcagag 1024











481 TTTTCTCATGGTCTTGGGCGATTTCAGGACACCTTTATTCCTGCTATTGGCATTCACCTGGC 540  
 605 tttttctcatggctcttggggcattcaggacacctttatctgctattggcattggacctggc 664  
 541 ATCTCATGGGTTTATGATTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTAA 600  
 665 atctcatgggtttatagttgctgtgtagaacacagagatagatctgcatctgcaactta 724  
 601 CTATTTCGAAGGACCAATCTCTGTCAGAAATAGGGACACAGCTCTTGGCTCTACCTTAGAAC 660  
 725 ctatttcaaggaccacactctgctcagaaa taggggacaagctcttggctctaccttagaac 784  
 661 CCTGAACAAGAGAGAGAGACACATATPACGAAATAGCAGGTTACGGCAAGAGCAAAAGA 720  
 785 cctgaacaagagagagagacacata Laqgaatagagcagggtacgggcaaaagagcaaaaga 844  
 721 ATGTTTCCCAAGCTCTCAGTCTGATGCTTGTGACATTTGATGATGATGATGATGATGATG 780  
 845 atgttcccaagctctcagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 904  
 781 ATTGAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840  
 905 attagatttaagtttgataggaacaactgaaggactctattgataggggaataatagc 964  
 841 AGTAATTTGAGACATTTTGTGGTGGAGCAAGGTTATTGACAGCTCTTATGATGATGATGATG 900  
 965 agtaattggacatttttggtaggaacaacgctctctcagactctttagtgaaga tcaag 1024  
 901 ATTGAGATTTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 1025 attcagatgggtattgctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 1084  
 961 CAGAATTTCTCAGCCCTCTCTTTTATCAACTCTGATATTTTCCCAATATCTCTGCTAATAT 1020  
 1085 cagaattctcagccctctcttttataactctggaatttcccaatctcctgctgctgctgct 1144  
 1021 CATTAATAATGAAATAATGCTACTCAGCTGATGATGATGATGATGATGATGATGATGATG 1080  
 1145 catataataataataataatgctactcactgataaagaagaagaatgattacacatcaggg 1204  
 1081 TTCAGTCCACGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 1205 ttcagtcacagaaatttgcgactctcacttttgcactgctgctgctgctgctgctgctgct 1264  
 1141 GCTCAATTAAGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
 1265 gcccaattaaaggaggagacatagattcctaagttagctattgatttagcacaagaagcttc 1324  
 1201 ATTGACATTTCTTACAAAAGCATTTAGGACTTTCATAAAGATTTTGTGATGATGATGATG 1260  
 1325 attagattcttcaaaaagcatttaggacttcataaagaattttgactagtgaggactgctt 1384  
 1261 GATTGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
 1385 gattgaaggagatgagagaa cctlatccaggggaccacacattacacacacacacacac 1444  
 1321 CATGATGTTACGAACCTCTCTCAGGAATAGAGAAATACAAATTT 1361  
 1445 catcatgttacgaactcttcagggaatagagaaatcacatt 1485

## RESULT 9

AAA59579

ID AAA59579 standard; cDNA; 1520 BP.

XX AAA59579;

AC AAA59579;

XX 14-NOV-2000 (first entry)

DT cDNA encoding plasma platelet-activating factor acetylhydrolase.

DE platelet-activating factor acetylhydrolase; platelet-activating factor;

XX reperfusion injury; acute inflammation; pleurisy; asthma;

KW

KW

necrotising enterocolitis; adult respiratory distress syndrome; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 162..1487  
 FT /\*tag= a  
 FT /product= "platelet-activating factor acetylhydrolase"  
 XX US6099836-A.  
 XX 08-AUG-2000.  
 XX 19-JUN-1998; 98US-0100546.  
 XX 07-JUN-1995; 95US-0480658.  
 XX 22-JAN-1998; 98US-0010715.  
 XX 06-OCT-1993; 93US-013803.  
 XX 06-OCT-1994; 94US-0318905.  
 XX (ICOS-) ICOS CORP.  
 XX Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;  
 PI Cousins LS;  
 XX WPI; 2000-531654/48.  
 XX DR P-PSDB; AAB07774.  
 XX PS Example 3; Column 45-48; 55pp; English.  
 XX CC The specification describes a pharmaceutical composition comprising  
 CC platelet-activating factor acetylhydrolase. The composition is  
 CC administered for treating a mammal susceptible to or suffering from  
 CC a platelet-activating factor-mediated condition associated with  
 CC reperfusion injury. Diseases and conditions which may be treated  
 CC include acute inflammation, pleurisy, asthma, necrotising enterocolitis  
 CC and adult respiratory distress syndrome. The present sequence encodes  
 CC human plasma platelet-activating factor acetylhydrolase.  
 XX SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 21; Length 1520;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGACAGACTAAGCTGAACCTGCTCAGCTCCACAGATGGTGCCACCAATTCGATGT 60  
 DB 125 tgagagactaaagctgaaactgctcagctcccaagatggtgccacccaaattgcatgt 184  
 QY 61 GCCTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 DB 185 gcttttctgctctgcggctgctgctgctgctgctgctgctgctgctgctgctgct 244  
 QY 121 TCCTGTTGCCCATATGAATATCATCAGCTGGGTGCACAAATACAAATGCTGATGCTGC 180  
 DB 245 tccctgtgcccataatgaatcatcagcatgggtccaaacaaatacagaactgctgctgc 304  
 QY 181 TGCAAGCTTTTGGCCAAACTAAAATCCCGGGGAAATGGCGCTTATTCGCTTGTGTGAC 240  
 DB 305 tgcaagcttttgccaaactaaaatccccggggaataaggccttattcctgctgctgac 364  
 QY 241 AGACTTAATGTTTGTATCAGACTAAATGAAGGACCTCTCTGCTTATATATATTCATCC 300  
 DB 365 agacttaattgttgcataactaaagaaggacacctctctgcttataataccatccca 424  
 QY 301 AGATATGATGCTGCTTGCACACCTTTGGATGCCCAATAAAGAAATATTTTGGGGTCTTAG 360  
 DB 425 agataatgacgccttgacaccccttggatcccaataaagaataatttttggggtcttag 484

QY	361	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT	420	XX	AC	AAA10861;
Db	485	caaatctcttggaacacactggtttagggcaacattttgaggttactcttggttcaat	544	XX	DT	14-JUL-2000 (first entry)
QY	421	GACAACTCTGCAAACTGGAATCCCTCTGAGCCCTGGTGAATAATATCCACTTCTTCT	480	XX	DE	Human platelet-activating factor acetyl hydrolase nucleotide sequence.
Db	545	gacaactctgcaactggaattcccccctggagccctggcgaataataatccacttgctt	604	XX	KW	platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;
QY	481	TTTTTCTCATGCTCTGGGGCATTCAGACACTTTATTCGTGATTTGGGATGACCTGGC	540	XX	KW	inflammatory response; pre-term labour; pharmaceutical composition;
Db	605	ttttctcatggtcttggggcattccaggacacactttattctgctattggcattgacctggc	664	XX	KW	regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease; ss;
QY	541	ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA	600	XX	OS	pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.
Db	665	atctcatgggtttatagttctgtctgttagaacacagagatagatctgcatctgcaactta	724	XX	OS	Homo sapiens.
QY	601	CHATTTCAGAGACCNAATCTGTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTGAAC	660	XX	Key	Location/Qualifiers
Db	725	ctattttcaaggaccatctgctgcagaatataggggacaagtcttggctctaccttagaac	784	XX	CDS	162..1487
QY	661	CTTGAACCAAGAGGAGGACACATATACGAAATGAGCAGGTACGCGAAAGAGCAAAAGA	720	XX	FT	/*tag= a
Db	785	cttgaacaaagaggagagacacatacgaatgagcaggtacgcgaagagcaaaaga	844	XX	FT	/product= PAF-AH
QY	721	ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATTTGATGATGATGGAAGCCAGTGAATGC	780	XX	FT	/note= "platelet-activating factor acetyl hydrolase"
Db	845	atgttcccaagctctcagctctgattcttggacattgacatggaagccagtgaggaatgc	904	XX	FN	US6045794-A.
QY	781	ATTAGATTTTAAAGTTTGAATATGGAACAACTCAAGGACTCTATTGATAGGGAATAATAGC	840	XX	PD	04-APR-2000.
Db	905	attagatttaagtgttatggaacaaactgaaggactclattgatgggaaaaaatagc	964	XX	PE	09-JUN-1999; 99US-0328474.
QY	841	AGTAATTTGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTATGTAAGATCAGAG	900	XX	PR	12-AUG-1997; 97US-0910041.
Db	965	agtaattggacattcttttggggagcaacggttattcagactctttagtggaatcagag	1024	XX	PR	06-OCT-1993; 93US-0133803.
QY	901	ATTGAGATGTTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	960	XX	PR	06-OCT-1994; 94US-0318905.
Db	1025	attcagatggttattgacctgagtgatgagtgatttccactgggtgatgaattatct	1084	XX	PR	07-JUN-1995; 95US-0483232.
QY	961	CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGATATTTTCAATATCTCTGCTAATAT	1020	XX	PA	(ICOS-) ICOS CORP.
Db	1085	cagaattctcagccctctcttttatacaactctgaaatttccaatatctcgtctaata	1144	XX	PI	Cousens LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
QY	1021	CATAAAATCAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACATCAGGGG	1080	XX	PI	Eberhardt CD;
Db	1145	cataaaaatgaaaaatgctactcaccigataaagaaagaaagatgattacaatcagggg	1204	XX	XX	WPI; 2000-282671/24.
QY	1081	TTGAGTCCACCAATTTTCTGCTTCTCCTTCTTCTGCACTGCACTGCACTGCACTGCACT	1140	XX	DR	P-PSDB; AAY88301.
Db	1205	ttagtccacagaaatttgcgtacttcttcttcttcttcttcttcttcttcttcttcttct	1264	XX	DR	Treatment of mammals suffering from pre-term labour comprises
QY	1141	GCTCAAAATTAAGGGAGACATAGATTCAAAATGACGCTATTGATCTTACCAACAAGCTTC	1200	XX	PT	administering a pharmaceutical composition comprising
Db	1265	gctcaaatataaggaggagacatagattcaaatgtagctattgattcttagcaacaagcttc	1324	XX	PT	platelet-activating factor acetyl hydrolase enzyme -
QY	1201	ATTAGCATTTCTTACAAAGCATTTTAGACTTCTTCAATTAAGATTTTGTGCTGGGACTGCTT	1260	XX	PS	Claim 1; Column 63-68; 67pp; English.
Db	1325	attagcattcttcaaaagcatttagagacttcaaaagattttagcagtgaggactgctt	1384	XX	CC	This sequence represents a nucleotide sequence encoding the human
QY	1261	GATTGAAGGAGATGATGAGATCTTTATCCAGGGACCAACATTAACACAACCAATCAACA	1320	XX	CC	platelet-activating factor acetyl hydrolase (PAF-AH). PAF is a
Db	1385	gattgaaggagatgatgagaaatttattccaggggacacatttaacacaaatcaaca	1444	XX	CC	phospholipid and is implicated in pathological inflammatory responses
QY	1371	CATCATCTTACAGAACTCTTCAGGAATAGAGAAATACRATT	1361	XX	CC	(e.g. asthma, anaphylaxis, septic shock and arthritis). PAF-AH is
Db	1445	catcatgttacagaactcttcaggaatagagaatacaatt	1485	XX	CC	released by hepatocytes, and macrophages and inactivates PAF. PAF-AH also
RESULT	10			XX	CC	inactivates oxidatively fragmented phospholipids that mediate
AAA10861				XX	CC	inflammation. This sequence is specifically claimed for use in a method
ID	AAA10861			XX	CC	to treat a mammal suffering from pre-term labour. PAF-AH is included in a
				XX	CC	pharmaceutical composition which can be administered to a mammal
				XX	CC	suffering from pre-term labour. The invention relates to purified and
				XX	CC	isolated polynucleotide sequences encoding human PAF-AH and materials and
				XX	CC	methods for the recombinant production of PAF-AH products which are
				XX	CC	expected to be useful in regulating inflammatory events. The
				XX	CC	administration of PAF-AH to animals may be used for ameliorating
				XX	CC	pathological inflammatory conditions such as asthma, anaphylaxis, shock,
				XX	CC	arthritis, Crohn's disease, pancreatitis, allergic inflammation, and
				XX	CC	human immunodeficiency virus (HIV).
				XX	CC	Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;
				XX	CC	Query Match 99.9%; Score 1359.4; DB 21; Length 1520;
				XX	CC	Best Local Similarity 99.9%; Pred. No. 0;
				XX	CC	Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
				QY	1	TCGAGACACTAAGCTCAAACTGCTGCTCAGCTCCCAAGATGTCGCCCAAAATTCGATGT
				Db	125	tgagagactaagctgaaactgctgctcagctcccaagatgggtgccaccccaaatgcatgt

[illegible]

QY	1141	GCTCAATTAAAGGAGACATAGATTCAAAATCAGCTATTGATCTTACCAACAAGCTTC	1200
Db	1265	gctcaattaaaggagacatagattccaattgagctattgatcttagcaaaaagcttc	1324
QY	1201	ATTAGCACTCTTACAAAGCATTTAGGACTTTCATAAAGATTTTGTATCAGTGGGACTGCTT	1260
Db	1325	attgactcttccaagaagcatttaggacttcataaagatttgatcagtgaggctgctt	1384
QY	1261	GATTGAAGGAGATGATCAGAATCTTATTCAGGGGACCAACATTTACACAACCAATCAACA	1320
Db	1385	gattgaaggagatgataagaattctattccagggcccaacatttaacacaaccaatcaaca	1444
QY	1321	CATCATGTTTACAGACTCTTTCAGGAATAGAGAAATACAAAT	1361
Db	1445	catcatgttacagaactcttcaggaataagaagaatacagaatt	1485

RESULT 11  
AAZ24240  
ID AAZ24240 standard; cDNA; 1520 BP.

XX  
AC  
AAZ24240:

XX  
DT 08-FEB-2000 (first entry)XX  
DE  
HUMAN RES-AU CONN

XX

KW  
antigen-activating factor acetylcholinesterase; PAF-AH; human; treatment

KW  
antiinflammatory; antiasthmatic; antiallergic; antiarthritic; asthma;

KW  
antischemic; inflammatory disorder; anaphylaxis; ulcerative colitis;

KW  
antigen-induced arthritis; ischemia; septicemia; allergy; ss.

XX	
OS	Homo sapiens

XX	Key	Location / Qualifications
FH		

FT CDS 162..1487

FT  
/product="PAF-AH"  
/product="PAF-AH"

XX  
PN  
US5977308-A.XX  
PD  
02-NOV-1999

XX  
DE 12-AUG-1967. 07HC-001001

	XX
	XX

PR 06-OCT-1994; 94US-0318905.  
00-OCT-1993; 95US-0133803.

PR 07-JUN-1995; 9505-0483232.  
XX

PA (ICOS-) ICOS CORP.  
YY

PI  
Cousens LS, Gray P, Trong HL, Tjo

XX  
LDCRMIGL CD,  

DR WPI; 2000-021956/02.  
DR P-PSDB; AAY50735.

Truncated and truncated  
XX PT

PT acetylhydrolase, for treating or pre

XX  
XX  
XXXXXX 0000XX  
FS  
CLAIM 9a; COLUMN 59-64; 65pp; ENGLISH

CC This invention describes novel truncated  
CC PAF-AH (platelet activating factor =

antiinflammatory, antiasthmatic, ant

inflammatory disorders, e.g. asthma,

CC  
CC  
CC  
CC  
CC

Recombinant (I), produced in prokaryotic system; ulcerative colitis, ischemic enteritis, prokaryotic system

CC at the terminus than the full-length  
CC versions also have greater activity

CC sequence encodes the human PAF-AH pr

100

CC method of the invention.

XX Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 21; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGAGACTAAGCTGAACCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCATGT 60  
 DB 125 TGAGAGCTAAGCTGAACCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCATGT 184  
 QY 61 GCTTTTCGCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 DB 185 GCTTTTCGCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244  
 QY 121 TCCCTGCTCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180  
 DB 245 TCCCTGCTCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 304  
 QY 181 TCCAGCTTTGGCCAAACTAAATCCCGCGGAATGGGCTTATTCGTTGGTGTAC 240  
 DB 305 TCCAGCTTTGGCCAAACTAAATCCCGCGGAATGGGCTTATTCGTTGGTGTAC 364  
 QY 241 AGACTTAATGTTGATCACACTAATAAGGCACTTCTTCCGCTTTATATATCCATCCCA 300  
 DB 365 AGACTTAATGTTGATCACACTAATAAGGCACTTCTTCCGCTTTATATATCCATCCCA 424  
 QY 301 ACATTAATGATCGCTTGACACCTTTCGATCCCAATTAAGAAATATTTGGGCTCTAG 360  
 DB 425 AGATAATGATCGCTTGACACCTTTCGATCCCAATTAAGAAATATTTGGGCTCTAG 484  
 QY 361 CAAATTTCTTGAACACACTGGCTTATGGCAACATTTTGGGCTTACCTGTTCAAT 420  
 DB 485 CAAATTTCTTGAACACACTGGCTTATGGCAACATTTTGGGCTTACCTGTTCAAT 544  
 QY 421 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTTGGTCAAAATATCCACTTGTGT 480  
 DB 545 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTTGGTCAAAATATCCACTTGTGT 604  
 QY 481 TTTTTCATGCTCTGGGGCACTTACGACACTTTTATTCGCTTATTTGGGCACTTACCTGGC 540  
 DB 605 TTTTTCATGCTCTGGGGCACTTACGACACTTTTATTCGCTTATTTGGGCACTTACCTGGC 664  
 QY 541 ATCTCATGCTTTATAGTTGCTGTGTAGACACAGAGATGATCTGCATCTGCAACTTA 600  
 DB 665 ATCTCATGCTTTATAGTTGCTGTGTAGACACAGAGATGATCTGCATCTGCAACTTA 724  
 QY 601 CTATTTCAAGGCACTTCTGCTGCAAAATAGGCGGCAAGCTTGGCTCTACCTTAGAAC 660  
 DB 725 CTATTTCAAGGCACTTCTGCTGCAAAATAGGCGGCAAGCTTGGCTCTACCTTAGAAC 784  
 QY 661 CCTGAACAAAGAGGAGGACACATATACGAATGAGGAGCTAGCGCAAGAGCAAAAGA 720  
 DB 785 CCTGAACAAAGAGGAGGACACATATACGAATGAGGAGCTAGCGCAAGAGCAAAAGA 844  
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGCAAGGCAAGCTGCAAGATGC 780  
 DB 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGCAAGGCAAGCTGCAAGATGC 904  
 QY 781 ATTAGATTTTAACTTTGATATGGAACACTGAAGGACTTATTTGATAGGGAATAATAGC 840  
 DB 905 ATTAGATTTTAACTTTGATATGGAACACTGAAGGACTTATTTGATAGGGAATAATAGC 964  
 QY 841 AGTAATTTGACATCTTTTGGGCAACGCTTATTCAGACTCTTACTGAGATCAGAG 900  
 DB 965 AGTAATTTGACATCTTTTGGGCAACGCTTATTCAGACTCTTACTGAGATCAGAG 1024  
 QY 901 ATTTCAGATGCTGTTTGGCTTGCATGCATGGATGTTTCCACTTGGGTGATGATATATTC 960  
 DB 1025 ATTTCAGATGCTGTTTGGCTTGCATGCATGGATGTTTCCACTTGGGTGATGATATATTC 1084

QY 961 CAGAAATCTCTAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATAT 1020  
 DB 1085 CAGAAATCTCTAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATAT 1144  
 QY 1021 CATAAAAATCAAAAAATGCTACTCTACCTGTATAAAGAAAGAAAGATGATTACATCAGGGG 1080  
 DB 1145 CATAAAAATCAAAAAATGCTACTCTACCTGTATAAAGAAAGAAAGATGATTACATCAGGGG 1204  
 QY 1081 TTCAGTCCACCAAGATTTGCTGACTTCTACCTTTTGGCAACTGGCAAAATATTTGACACAT 1140  
 DB 1205 TCCAGTCCACCAAGATTTGCTGACTTCTACCTTTTGGCAACTGGCAAAATATTTGACACAT 1264  
 QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCACTTATTTGATCTTACCAACAAAGCTTC 1200  
 DB 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCACTTATTTGATCTTACCAACAAAGCTTC 1324  
 QY 1201 ATTAGCATTTCTTACAAAACATTTAGGACTTTCATTAAGATTTTGTATCAGTGGGACTGCTT 1260  
 DB 1325 ATTAGCATTTCTTACAAAACATTTAGGACTTTCATTAAGATTTTGTATCAGTGGGACTGCTT 1384  
 QY 1261 GATTGAAGGAGATGATGAAATCTTTATTTCCAGGAGCAACATTTACCAACCAATCAACA 1320  
 DB 1385 GATTGAAGGAGATGATGAAATCTTTATTTCCAGGAGCAACATTTACCAACCAATCAACA 1444  
 QY 1321 CATCATGTTTACAGAACTTCTTACGGAATAGAGAAATACAAAT 1361  
 DB 1445 CATCATGTTTACAGAACTTCTTACGGAATAGAGAAATACAAAT 1485

RESULT 12  
 AAD04143  
 ID AAD04143 standard; cDNA; 1520 BP.

XX AAD04143;

XX 02-JUL-2001 (first entry)

Human plasma platelet-activating factor acetylhydrolase (PAF-AH) cDNA.  
 Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
 antiinflammatory; septicaemia; inflammation; haemostasis; parturition;  
 asthma; anaphylaxis; septic shock; antibacterial; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 CDS 162..1487

FT /\*tag= a  
 FT /product= "Human platelet-activating factor  
 FT acetylhydrolase (PAF-AH) protein"  
 FT 162..284

FT sig\_peptide

FT /\*tag= b  
 FT /note= "This region contains 162-212 bases of signal  
 FT sequence and 213-284 bases encoding an additional peptide  
 FT that is cleaved to yield the mature functional enzyme"  
 FT 285..1484

FT mat\_peptide

FT /\*tag= c  
 FT /product= "Mature human platelet-activating factor  
 FT acetylhydrolase (PAF-AH) protein"

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

XX 22-JAN-1998; 98US-0010715.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX

PI	Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI	Wilder CL;
XX	
DR	WPI; 2001-280610/29.
DR	P-PSDB; AAE00761.
XX	
PT	Treating a mammal susceptible to or suffering from septicemia comprises
PT	administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT	supplement endogenous PAF-AH activity and to inactivate pathological
XX	amounts of PAF -
PS	Claim 1: Column 43-48; 54pp; English.
XX	
CC	The present cDNA sequence encodes human plasma platelet-activating factor
CC	acetylhydrolase (PAF-AH) protein.
CC	The invention relates to human plasma platelet-activating factor
CC	acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
CC	invention also relates to method of treating a mammal susceptible to
CC	or suffering from septicemia. PAF functions in normal physiological
CC	processes such as inflammation, haemostasis and parturition. PAF-AH
CC	specific antibodies are used in the diagnostic methods to detect abnormal
CC	levels of PAF-AH in serum and also for treating the pathological
CC	inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
CC	shock and arthritis. PAF-AH antibody is also useful for screening a
CC	genetic lesion in the human plasma PAF-AH gene, which occurs due to the
CC	replacement of nucleotide G to T at position 996 within exon 9 resulting
CC	in replacement of amino acid Val to Phe at position 279. Thus the
CC	deficiency of PAF-AH activity is due to the genetic lesion in human
XX	plasma PAF-AH gene.
XX	
SQ	Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match	99.9%;	Score 1359.4;	DB 22;	Length 1520;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1360;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;

QY	1	TCAGAGACTAGCTGAACACTGCTGCTCAGCTCCCAAGATGGTGGCCACCAATATGCCATGT	60
Db	125	tgagagactaagctgaactgtctcagctcccaagatggcgccacccaattgcattgt	184
QY	61	GCTTTTCTGCTCTGCGGCTGCTTGGTGTATCCCTTTTCAGCTGGCAATACATAAA	120
Db	185	gctttctgctctgcggtgctgtgtgtttacctcttgcactggccaatacaaaa	244
QY	121	TCCGTGTTGCCATATGAATCATCAGCATGGGTCAACAAATACAACTACTGATGGCTGC	180
Db	245	tccgtgtgcccataatgaataatcagcatgggtgccaacaaatacaagtactgaaggctgc	304
QY	181	TGCAAGCTTTGGCCAAACTAAATCCCGGGGAATGGCGCTTATTCGGTGGTGTCTAC	240
Db	305	tgaagctttggccaaactaaaatccccggggaaatgggcccattccgttgggtgtac	364
QY	241	AGACTTAATCTTGCATCACACTAATAGGGCACCTCTTGGCTTTATATATCCATCCCA	300
Db	365	agacttaattgttgatcacactaataaggcgacactcttgcgtttatattatccatccca	424
QY	301	AGATAATGATGCGCTTGACACCCCTTTGGATCCCAAAATAAAGAAATATTTTGGGGTCTTAG	360
Db	425	agataatgatcgcccttgacacccctttggatcccccaataaagaataattttggggctctag	484
QY	361	CAAAATTTCTGGAAACACATGGCTTATGGCCACATTTGAGGTTTACTCTTTGGTTCAT	420
Db	485	caaatctctggaaacacactggcttatgggcaacatttggagttactctcttgggttcaat	544
QY	421	GACAACCTCTGCAACTGGAAATTCCTCCTCTGAGCGCTGGTGAAAAATATCCCACTGTGTG	480
Db	545	gacaactctcgaaactggaaattccccctctgagggctggtgaaaaataaccacttgtgt	604
QY	481	TTTTTCTCATGCTTTGGGGCATTCAGGACACTTATTCGTATTTGGCATGACCTGGC	540
Db	605	tttttctcatggtcttggggcaattccaggacatttattctgtatttggcatgacctggc	664

PN US6146625-A.  
 XX 14-NOV-2000.  
 XX 22-JAN-1998; 98US-0010715.  
 XX 07-JUN-1995; 95US-0480658.  
 PR 06-OCT-1993; 93US-0133803.  
 PR 06-OCT-1994; 94US-0318905.  
 XX (ICOS-) ICOS CORP.  
 XX Gray P, Trong HL, Tjoelker LW, Wilder CL, Eberhardt CD;  
 PI Cousins LS;  
 DR P-PSDI; 2001-040421/05.  
 DR WPI; AAB49451.  
 XX Treating platelet-activating factor mediated pathologies such as  
 PT asthma, rhinitis, pleurisy and acute respiratory distress syndrome  
 PT comprising administering platelet-activating factor acetylhydrolase  
 PT enzyme  
 XX Claim 1; Column 45-48; 54pp; English.  
 XX The present invention relates to a method for treating a mammal  
 CC susceptible to or suffering from a platelet-activating factor  
 CC (PAF)-mediated pathological condition, comprising administering a  
 CC composition comprising PAF acetylhydrolase (PAF-AH) enzyme to  
 CC supplement endogenous PAF-AH activity and to inactivate pathological  
 CC amounts of PAF in the mammal. PAF-mediated pathological conditions  
 CC are conditions such as pleurisy, asthma, rhinitis, necrotizing  
 CC enterocolitis and acute respiratory distress syndrome in mammals.  
 CC The present sequence is the coding sequence for human PAF-AH.  
 XX Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;  
 SQ  
 Query Match 99.9%; Score 1359.4; DB 22; Length 1520;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCAGAGTGTGCGCCACCAATTCGATGT 60  
 DB 125 tgagagactaagctgaactgctgctcagctccagatggtgcccacccaactgcaagt 184  
 QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 DB 185 gcttttctgctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244  
 QY 121 TCCTGTGCTCCATATGAAATCAGATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 DB 245 tccgtgtgctccatataatgaaatcagatggtgcccacccaactgcaagtgtgctgctgct 304  
 QY 181 TGCAAGCTTTGGCCCAACTAAATPCCCGGGGAAATGGGCGCTTATTCGTTGTTGTAC 240  
 DB 305 tgcagctttggcccaactaaaatcccccggggaatggcgcttattccgctgtgtgtgctac 364  
 QY 241 AGACTTAATGTTTTCATCAGCTTAATAGGCGCTTCTTTCGCTTATATATATTCATCCCA 300  
 DB 365 agacttaatgtttcatcagcttaataagggcaactcttctgcttattatccatccca 424  
 QY 301 AGATAATGATCGCTTGACACCTTTTGATGCTCCCAATTAAGATATATTTTGGGGCTTAG 360  
 DB 425 agataatgctgtgacaccccttggatcccaataaagaataatttttggggcttag 484  
 QY 361 CAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTCAGCTTACTCTTTGGTTCAAT 420  
 DB 485 caaatctcttggaaacacactggcttattgggcaacatttggagttactcttggttcaat 544  
 QY 421 GACAACTCCTGCAACTGGAATCCCTCTGAGGCTGGTGAATAATATCCACTTCTGCT 480  
 DB 545 gacaaactcctgcaactggaatccctctgagggcctggtgaaaaatataccacttggct 604  
 QY 481 TTTTCTCATTGGTCTTGGGCACTTCAGAGACATTTATTTCTGCTATTGGCATTGACCTGGC 540  
 DB 605 ttttctcattggcttggggcattcaggacactttattctgtattgttgattgacctggc 664  
 QY 541 ATCTCATGGGTTTATAGTTGCTGCTCTAGAACACAGAGATAGATCTGCTGCAACTTA 600  
 DB 665 atctcatgggtttatagttgctctgtagaacacagagatagatctgcatctgcaactta 724  
 QY 601 CTATTTCAAGGACCAATCTGCTGACAAATAGGGGACAAAGTCTTGGCTCTTACTTTAGAAC 660  
 DB 784 ctatttcaaggacccaatctgctgacaaataggggacaagtctggctctactcttagaac 784  
 QY 661 CCTGAAACAAGAGAGAGAGACACATATACAAATGACAGGTACGGCAAGACAAAGA 720  
 DB 844 cctgaaacaagagagagagacacatacgaatgacaggttacggcaaaagacaaaga 844  
 QY 721 ATGTTTCCCAAGCTCTCAGTCTGATTTGATTCATGATTCATGGAAGCCAGTGAAGAATGC 780  
 DB 904 atgttcccaagctctcagctctgattcttgacattgatcatggaagccagtgaaagtgc 904  
 QY 781 APTAGATTTAAAGTTTGATATGGAACCACTGAAGGACTCTATTGATAGGGAANAATAGC 840  
 DB 964 attagattaaagtgtgatggaacaactgaaggactctattgtaggggaaaaaatagc 964  
 QY 841 AGTAATTCGACATTTCTTTGTTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900  
 DB 1024 agtaattcgacattcttttggtagcaacggttattcagaactctttagtgaagatccagag 1024  
 QY 901 ATTCAGATGCTGGTATTTGCCCTGGGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 1084 attcagatgctggtattgcccctggatgcatggtgttccactggtggtgaaagtattatc 1084  
 QY 961 CAGAATTCCTCAGGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTGCTGCTAATAT 1020  
 DB 1144 cagaattcctcagccctctttttatcaactctgaaattttccaatctctgctaatat 1144  
 QY 1021 CATAAATTAAGAAATGCTACTCAGCTGATTAAGAAAGAAAGATGATTAACAATCAGGG 1080  
 DB 1204 cataaaatgaaaatgctactcaccctgataaaagaaagaaagatgattacaatccaggg 1204  
 QY 1081 TTCAGTCCACCAAGATTTTGTGCTGCTTCCACTGTCGCACTGGGCAAAATATTTGACACAT 1140  
 DB 1264 ttcagtccaccagaatttggctgacttcttggcaacttggcaaaaataattggacacat 1264  
 QY 1141 GCTCAATTTAAAGGAGACATAGATTTCAAAATGCACTTATTCATCTTACCAACAAAGCTTC 1200  
 DB 1324 gctcaatttaaaggagacacatagattccaaatgtagctattgactcttagcaacaagcttc 1324  
 QY 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTTAGGACTTTAGGACTTTAGGACTTTAGGACT 1260  
 DB 1384 attagcatcttaccaaaagcatttaggacttcaaaagatttggatcagtgggacgctt 1384  
 QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACCAACCAATCAACA 1320  
 DB 1444 gattgaaggagatgatgaaatcttattccagggacccaacattacaacacacacacac 1444  
 QY 1321 CATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361  
 DB 1485 catcatgttacagaactcttcagggaatagagaatacacaatt 1485  
 RESULT 14  
 AAT63701  
 ID AAT63701 standard; cDNA; 1520 BP.  
 XX  
 AC AAT63701;  
 XX  
 DT 12-JUN-1997 (first entry)  
 XX cDNA encoding platelet-activating factor acetylhydrolase.  
 XX Human platelet-activating factor acetylhydrolase; PAF-AH; detection;  
 KW









Search completed: March 8, 2002, 23:08:27  
Job time: 3900 sec



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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38.
US-08-557-892-9

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Query Match	Score 1361;	DB 2;	Length 1361;
Best Local Similarity	100.08;		
Best Local Similarity	100.08;		

	Matches	1361;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
OY	1	TGAGAGACTAAGCTGAACCTGCCTCCTCAGCTCCCAAGATGGTGGCACCCAATAATTCGATGT	60						
Db	1	TGAGAGACTAAGCTGAACCTGCCTCCTCAGCTCCCAAGATGGTGGCACCCAATAATTCGATGT	60						
OY	61	GCTTTTCTGCCCTCGCGGCTGCCTGGCTGTGGTTATCCTTTTGACCTGGCAATACATAAA	120						
Db	61	GCTTTTCTGCCCTCGCGGCTGCCTGGCTGTGGTTATCCTTTTGACCTGGCAATACATAAA	120						
OY	121	TCCTGTTGCCCATATGAAGAATCATCAGCATGGTCAACAATAATACAAGTACTGATGGCTGC	180						
Db	121	TCCTGTTGCCCATATGAAGAATCATCAGCATGGTCAACAATAATACAAGTACTGATGGCTGC	180						
OY	181	TGCAAGCTTTGSCCAAACTAAAAATCCCCGGGGGAANTGGCCTTAATCCGTTGGTTGTAC	240						
Db	181	TGCAAGCTTTGSCCAAACTAAAAATCCCCGGGGGAANTGGCCTTAATCCGTTGGTTGTAC	240						
OY	241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTCTCTTGGGTTTTATATTATCCATCCCCA	300						
Db	241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTCTCTTGGGTTTTATATTATCCATCCCCA	300						
OY	301	AGATAATCATCGCCTTCACACCCTTTGGATCCCANAATAAAGNAATATTTTTGGGGTCTTAG	360						
Db	301	AGATAATCATCGCCTTCACACCCTTTGGATCCCANAATAAAGNAATATTTTTGGGGTCTTAG	360						
OY	361	CAAATTTCTTGGAACACACACTGGCTTATAGGGCAACACTTTTGAGGTTACTCTTTGGTTCAAT	420						
Db	361	CAAATTTCTTGGAACACACACTGGCTTATAGGGCAACACTTTTGAGGTTACTCTTTGGTTCAAT	420						
OY	421	GACAACTCTCGCAACCTGGAATTTCCCTCTGAGGCGCTGGTGAANAATATCCACTTGTGT	480						
Db	421	GACAACTCTCGCAACCTGGAATTTCCCTCTGAGGCGCTGGTGAANAATATCCACTTGTGT	480						
OY	481	TTTTTCTCATGCTCTGGGGCAATTCAGGACACTTTATTTCTGCTATTTGGCATTCACCTGGC	540						
Db	481	TTTTTCTCATGCTCTGGGGCAATTCAGGACACTTTATTTCTGCTATTTGGCATTCACCTGGC	540						
OY	541	ATCTCATGGGTTTATAGTCTGCTGTAGAACACAGATAGATCTGCATCTGCCACTTTA	600						
Db	541	ATCTCATGGGTTTATAGTCTGCTGTAGAACACAGATAGATCTGCATCTGCCACTTTA	600						
OY	601	CTATTTCAAGSACCAATCTCTGTCAGAAATAGGGGACAAGTCTTTGGCTCTACCTTAGAAC	660						
Db	601	CTATTTCAAGSACCAATCTCTGTCAGAAATAGGGGACAAGTCTTTGGCTCTACCTTAGAAC	660						
OY	661	CCTGAAACAGAGGAGGACACATATACGAAATGACAGAGTACGGCAAGACAAAGA	720						
Db	661	CCTGAAACAGAGGAGGACACATATACGAAATGACAGAGTACGGCAAGACAAAGA	720						
OY	721	ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCGCTGAAGATGC	780						
Db	721	ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCGCTGAAGATGC	780						
OY	781	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGCACTTATTGTATAGGGAATAATAGC	840						
Db	781	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGCACTTATTGTATAGGGAATAATAGC	840						
OY	841	AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAG	900						
Db	841	AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAG	900						
OY	901	ATTGAGATGTGGTTATTTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTC	960						
Db	901	ATTGAGATGTGGTTATTTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTC	960						

Qy	961	CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTCCAAATATCTGCTAAATAT	1020
Db	961	CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTCCAAATATCTGCTAAATAT	1020
Qy	1021	CATAAAAATGAAAAATGCTACTCACCTGATAAGAAAGAAGATGATTACAATCAGGG	1080
Db	1021	CATAAAAATCAAAAAATGCTACTCACCTGATAAGAAAGAAGATGATTACAATCAGGG	1080
Qy	1081	TTCAAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAAATGGACACAT	1140
Db	1081	TTCAAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAAATGGACACAT	1140
Qy	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGGTTTC	1200
Db	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGGTTTC	1200
Qy	1201	ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACATGCTTT	1260
Db	1201	ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACATGCTTT	1260
Qy	1261	GATTGAAGGAGATGATGAGAACTCTATTTCAGGGACCAACAATTAACAACAACCAATCAACA	1320
Db	1261	GATTGAAGGAGATGATGAGAACTCTATTTCAGGGACCAACAATTAACAACAACCAATCAACA	1320
Qy	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATTT	1361
Db	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATTT	1361

```

RESULT 2
US-08-387-858A-9
; Sequence 9, Application US/08387858A
; Patent No. 5981252
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858A
; FILING DATE: 24 February 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

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Qy	1	TGAGAGACTAAGCTGAACCTGCTGCACCTCCCAAGAATGTCGCCACCAGAAATTCGATGT	60
Db	1	TGAGAGACTAAGCTGAACCTGCTGCACCTCCCAAGAATGTCGCCACCAGAAATTCGATGT	60
Qy	61	GCTTTTCTGCCTCTCGGGCTGCCTGGCTTGCTTTATCCTTTTCTGACTGGCAATACATAAA	120
Db	61	GCTTTTCTGCCTCTCGGGCTGCCTGGCTTGCTTTATCCTTTTCTGACTGGCAATACATAAA	120
Qy	121	TCCTGTGCCCATATGAATATCATACGATGGGTCAACAANAATACAAGTACTGATGCTGCG	180
Db	121	TCCTGTGCCCATATGAATATCATACGATGGGTCAACAANAATACAAGTACTGATGCTGCG	180
Qy	181	TGCAAGCTTTTGGCCAAAACTAANAATCCCCGGGGAAATGGGCTTTATTCCGTTGCTTGTAAC	240
Db	181	TGCAAGCTTTTGGCCAAAACTAANAATCCCCGGGGAAATGGGCTTTATTCCGTTGCTTGTAAC	240
Qy	241	AGACHTAATGTTTTGATCACACTAATAAGGGACCTCTTCGTGGTTATATTATCCATCCCA	300
Db	241	AGACHTAATGTTTTGATCACACTAATAAGGGACCTCTTCGTGGTTATATTATCCATCCCA	300
Qy	301	AGATAATGATCGCCTTGACACCCCTTTTGGATCCCAAATAAAGAATATTTTTGGGCTCTTAG	360
Db	301	AGATAATGATCGCCTTGACACCCCTTTTGGATCCCAAATAAAGAATATTTTTGGGCTCTTAG	360
Qy	361	CAAATTTCTTGGAACACACTTGGCTTATGGGCACACTTTTGAGGTACTCTTTGGTTCAAT	420
Db	361	CAAATTTCTTGGAACACACTTGGCTTATGGGCACACTTTTGAGGTACTCTTTGGTTCAAT	420
Qy	421	GACAACTCCTGCAAACTGGAAATCCCCTCTGAGGCTGGTGAANAATATCCACTTGTGT	480
Db	421	GACAACTCCTGCAAACTGGAAATCCCCTCTGAGGCTGGTGAANAATATCCACTTGTGT	480
Qy	481	TTTTTCTCATGGTCTTGGGCACTTCAGGACACTTTATTCTGCTATTGGCATTCAGCTGGC	540
Db	481	TTTTTCTCATGGTCTTGGGCACTTCAGGACACTTTATTCTGCTATTGGCATTCAGCTGGC	540
Qy	541	ATCTCATGGTTTATAGTTGCTGCTGTAGAACAACAGATAGATCTGCATCTGCAACTTA	600
Db	541	ATCTCATGGTTTATAGTTGCTGCTGTAGAACAACAGATAGATCTGCATCTGCAACTTA	600
Qy	601	CTATTTCAAGNCCAATCTGCTGCAGNAATAGGGNACRAGCTTTGGCTCTACCTTAGAC	660
Db	601	CTATTTCAAGNCCAATCTGCTGCAGNAATAGGGNACRAGCTTTGGCTCTACCTTAGAC	660
Qy	661	CTTGAAACAAGAGGAGGACACATATACCAATGAGCAGGTACGGCAAGAGCAAAAGA	720
Db	661	CTTGAAACAAGAGGAGGAGACATATACCAATGAGCAGGTACGGCAAGAGCAAAAGA	720
Qy	721	ATGTTTCCCAAGCTCTCAGTCTGATTTCTTGCATATGATCATNGAAGCCAGCTGAAGATGC	780
Db	721	ATGTTTCCCAAGCTCTCAGTCTGATTTCTTGCATATGATCATNGAAGCCAGCTGAAGATGC	780
Qy	781	ATTAGATTTAAAGTTTGTATGGSAACTTGAAGGACTCTATTGATAGGGAAAAAATAGC	840
Db	781	ATTAGATTTAAAGTTTGTATGGAACAACTTGAAGGACTCTATTGATAGGGAAAAAATAGC	840

NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1361 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 38...1360  
US-09-294-384B-9

Query Match 100.0%; Score 1361; DB 4; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTCCACCCCAAAATGGATGT 60  
Db 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTCCACCCCAAAATGGATGT 60  
Qy 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Qy 121 TCCCTGTTGCCCATATGAATATCATCAGCATGGTCAACAAATACAAATACAAATACAAAT 180  
Db 121 TCCCTGTTGCCCATATGAATATCATCAGCATGGTCAACAAATACAAATACAAATACAAAT 180  
Qy 181 TCGAAGCTTTGGCCAACTAAATCCCGCCGGGAAATGGGCCCTTATTCCTGTTGGTTGTAC 240  
Db 181 TCGAAGCTTTGGCCAACTAAATCCCGCCGGGAAATGGGCCCTTATTCCTGTTGGTTGTAC 240  
Qy 241 AGACTTAATGTTGATCACACTAATAGGCGACCTTCTTGGCGTTTATATATCCATCCCA 300  
Db 241 AGACTTAATGTTGATCACACTAATAGGCGACCTTCTTGGCGTTTATATATCCATCCCA 300  
Qy 301 AGATAATGATCGCTTCACACCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 360  
Db 301 AGATAATGATCGCTTCACACCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 360  
Qy 361 CAAATTTCTTGGAAACACTGGCTTATGGGCAACATTTTTCAGGTTACTCTTTGGTTCAAT 420  
Db 361 CAAATTTCTTGGAAACACTGGCTTATGGGCAACATTTTTCAGGTTACTCTTTGGTTCAAT 420  
Qy 421 GACAACCTCCGCAAACTGGAAATCCCTCTGAGGCTGCTGGAATAATATCCACTTGTGT 480  
Db 421 GACAACCTCCGCAAACTGGAAATCCCTCTGAGGCTGCTGGAATAATATCCACTTGTGT 480  
Qy 481 TTTTCTCATGCTTTGGGCAATTCAGGACACTTTATTCGCTATTGGCATTTGACCTGGC 540  
Db 481 TTTTCTCATGCTTTGGGCAATTCAGGACACTTTATTCGCTATTGGCATTTGACCTGGC 540  
Qy 541 ATCTCATGGTTTATAGTTGCTGCTAGAACACAGATAGATCTGCATCTGCAACTTA 600  
Db 541 ATCTCATGGTTTATAGTTGCTGCTAGAACACAGATAGATCTGCATCTGCAACTTA 600  
Qy 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGACAGTCTTGGCTCTACCTTAGAAC 660  
Db 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGACAGTCTTGGCTCTACCTTAGAAC 660  
Qy 661 CCTGAAACAGAGGAGGACACATATAGGAATGAGGAGTACGGCAAGAGCAAAAGA 720  
Db 661 CCTGAAACAGAGGAGGACACATATAGGAATGAGGAGTACGGCAAGAGCAAAAGA 720

Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATGAAAGCCAGTGAAGAATGC 780  
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATGAAAGCCAGTGAAGAATGC 780  
Qy 781 ATTAGATTTAAAGTTTGATATGCAACAACTGAAGCACTCTATTGATAGGGAAAAAATAGC 840  
Db 781 ATTAGATTTAAAGTTTGATATGCAACAACTGAAGCACTCTATTGATAGGGAAAAAATAGC 840  
Qy 841 ACTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTAGAGATCAGAG 900  
Db 841 ACTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTAGAGATCAGAG 900  
Qy 901 ATTCAGATCTGCTATTGCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTC 960  
Db 901 ATTCAGATCTGCTATTGCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTC 960  
Qy 961 CAGAATTCCTCAGCCCTCTTTTATCACTCTGAATATTTTCCAATATCTCTGCTAATAT 1020  
Db 961 CAGAATTCCTCAGCCCTCTTTTATCACTCTGAATATTTTCCAATATCTCTGCTAATAT 1020  
Qy 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080  
Db 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080  
Qy 1081 TTCAGTCCACAGAAATTTTGTGCTGCTTTCACCTTTTGGCACTTTTGGCACTTTTGGCACT 1140  
Db 1081 TTCAGTCCACAGAAATTTTGTGCTGCTTTCACCTTTTGGCACTTTTGGCACTTTTGGCACT 1140  
Qy 1141 GCTCAAAATTAAGGGAGACATAGATTTCAATGTCAGCTATTGATCTTACCAACAAGCTTC 1200  
Db 1141 GCTCAAAATTAAGGGAGACATAGATTTCAATGTCAGCTATTGATCTTACCAACAAGCTTC 1200  
Qy 1201 ATTAGCATTTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1260  
Db 1201 ATTAGCATTTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1260  
Qy 1261 GATTGAAGGAGATGATGAGAACTTTTATTCAGGCAACCAACATTAACACAACCAATCAACA 1320  
Db 1261 GATTGAAGGAGATGATGAGAACTTTTATTCAGGCAACCAACATTAACACAACCAATCAACA 1320  
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAATTT 1361  
Db 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAATTT 1361

RESULT 4  
us-08-470-187-7  
Sequence 7, Application us/08470187  
Patent No. 5532152  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine E.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gertlein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,187

FILING DATE: 435  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5532152and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 162..1484  
US-08-470-187-7

Query Match 99.9%; Score 1359.4; DB 1; Length 1520;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTCATGT 60  
DB 125 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTCATGT 184  
QY 61 GCTTTTCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 185 GCTTTTCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244  
QY 121 TCCTGTTGCCCATATGAATATCATCAGCATGGGTCAACAATAACAACTACTGATGCTGC 180  
DB 245 TCCTGTTGCCCATATGAATATCATCAGCATGGGTCAACAATAACAACTACTGATGCTGC 304  
QY 181 TCGAAGCTTTGGCCAACTAAATCCCGGGGAAATGGCCCTTATTCGCTGCTGCTGCTGCTGCT 240  
DB 305 TCGAAGCTTTGGCCAACTAAATCCCGGGGAAATGGCCCTTATTCGCTGCTGCTGCTGCTGCT 364  
QY 241 AGACTTAATGTTTATGATCAGCTAATAAGGCGACCTCTCTTGGCGTTATATATATCCATCCA 300  
DB 365 AGACTTAATGTTTATGATCAGCTAATAAGGCGACCTCTCTTGGCGTTATATATATCCATCCA 424  
QY 301 AGATAATGATCGCTTGCACACCTTTGGATCCCAATAAAGATATTTTGGGCTCTTAC 360  
DB 425 AGATAATGATCGCTTGCACACCTTTGGATCCCAATAAAGATATTTTGGGCTCTTAC 484  
QY 361 CAAATTTCTTGGAAACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420  
DB 485 CAAATTTCTTGGAAACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544  
QY 421 GACAACTCTGCAAACTGGAATCCCTCTGAGCCCTGGTGAATAATATCCATGCTGCT 480  
DB 545 GACAACTCTGCAAACTGGAATCCCTCTGAGCCCTGGTGAATAATATCCATGCTGCT 604  
QY 481 TTTTCTCATGCTTTGGGCAATTCAGACACATTTATCTGCTATTTGGGATTCACCTGGC 540  
DB 605 TTTTCTCATGCTTTGGGCAATTCAGACACATTTATCTGCTATTTGGGATTCACCTGGC 664  
QY 541 ATCTCATGGGTTATAGTTGCTGCTGTAGAACACAGATAGATCTGCTCTGCAACTTA 600  
DB 665 ATCTCATGGGTTATAGTTGCTGCTGTAGAACACAGATAGATCTGCTCTGCAACTTA 724  
QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGACAACTCTTGGCTCTACCTTGAAC 660  
DB 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGACAACTCTTGGCTCTACCTTGAAC 784

QY 661 CCTGAACAAGAGGAGGAGACACATATACGAATGACAGGTACGGCAAGACCAAGA 720  
DB 785 CCTGAACAAGAGGAGGAGACACATATACGAATGACAGGTACGGCAAGACCAAGA 844  
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTCATGGAAGCCATGGAAGATGC 780  
DB 845 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTCATGGAAGCCATGGAAGATGC 904  
QY 781 ATTAGATTTAAAGTTTGTATATGGAACAACCTGAAGSACTCTATTGATAGGGAATAATAGC 840  
DB 905 ATTAGATTTAAAGTTTGTATATGGAACAACCTGAAGSACTCTATTGATAGGGAATAATAGC 964  
QY 841 AGTAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTCAGTGAAGATCAGAG 900  
DB 965 AGTAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTCAGTGAAGATCAGAG 1024  
QY 901 ATTTCAGATGCTGATTTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 1025 ATTTCAGATGCTGATTTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084  
QY 961 CAGATTTCTCAGCCCCCTCTTTTTCATCACTCTGATATTTTCCCAATATCTTTCCTATATAT 1020  
DB 1085 CAGATTTCTCAGCCCCCTCTTTTTCATCACTCTGATATTTTCCCAATATCTTTCCTATATAT 1144  
QY 1021 CATTAATAATGAAAAATGCTACTCAGCTGATAAAGAAAAAGATGATTACAATCAGGGG 1080  
DB 1145 CATTAATAATGAAAAATGCTACTCAGCTGATAAAGAAAAAGATGATTACAATCAGGGG 1204  
QY 1081 TTCAGTCCACAGAAATTTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
DB 1205 TTCAGTCCACAGAAATTTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264  
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGACGCTATTGATCTTAGCAACAAGCTTC 1200  
DB 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGACGCTATTGATCTTAGCAACAAGCTTC 1324  
QY 1201 ATTAGCATTTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCATGCTGAGGACTGCTT 1260  
DB 1325 ATTAGCATTTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCATGCTGAGGACTGCTT 1384  
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTTACCAACAACCAATCAACA 1320  
DB 1385 GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTTACCAACAACCAATCAACA 1444  
QY 1321 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361  
DB 1445 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 5  
US-08-318-905-7  
Sequence 7, Application US/08318905  
Patent No. 5641669  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
NUMBER OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/318,905  
APPLICATION NUMBER: US/08/318,905  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5641669and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 162..1484  
US-08-318-905-7

Query Match 99.9%; Score 1359.4; DB 1; Length 1520;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAGCTGAACGCTGCTCAGCTCCAGATGCTGCCACCCCAAAATGTCATGT 60  
Db 125 TGAGAGACTAGCTGAACGCTGCTCAGCTCCAGATGCTGCCACCCCAAAATGTCATGT 184  
Qy 61 GCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 185 GCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184  
Qy 121 TCCTGTTGCCATATGAATATCATCAGCATGGTCAACAATACAGTACTGATGCTGCTGCTGCT 180  
Db 245 TCCTGTTGCCATATGAATATCATCAGCATGGTCAACAATACAGTACTGATGCTGCTGCTGCT 304  
Qy 181 TCGAAGCTTTGGCCAACTAAATATCCCGGGGAAATGGGCTTATTCGCTTGGTGTGAC 240  
Db 305 TCGAAGCTTTGGCCAACTAAATATCCCGGGGAAATGGGCTTATTCGCTTGGTGTGAC 364  
Qy 241 AGACTTAATGTTGATCACACTAATAGGSCACTTCTGCGTTTATATATATATATATATATATAT 300  
Db 365 AGACTTAATGTTGATCACACTAATAGGSCACTTCTGCGTTTATATATATATATATATATATAT 424  
Qy 301 AGATATATGCTGCTTGACACCTTTGGATGCCAAATAAAGAAATATTTTGGGGCTTAG 360  
Db 425 AGATATATGCTGCTTGACACCTTTGGATGCCAAATAAAGAAATATTTTGGGGCTTAG 484  
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGTACTCTTTGGTTCAT 420  
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGTACTCTTTGGTTCAT 544  
Qy 421 GACAACCTCGCAACTGGAATTCCTCTGAGGCTGCTGAGGAAATATFCCACTTGTGT 480  
Db 545 GACAACCTCGCAACTGGAATTCCTCTGAGGCTGCTGAGGAAATATFCCACTTGTGT 604  
Qy 481 TTTTCTCTATGCTTGGGGCACTTCAGGACCTTTATCTGCTATTGGCATTGACCTGGC 540  
Db 605 TTTTCTCTATGCTTGGGGCACTTCAGGACCTTTATCTGCTATTGGCATTGACCTGGC 664  
Qy 541 ATCTCATGGTTTATAGTTCCTCTAGAACACAGATAGATCTGCTGCAACTTTA 600

Db 665 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTGCAACCTTA 724  
Qy 601 CTATTTCAAGSACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGCTCTACCTTTAGAAC 660  
Db 725 CTATTTCAAGSACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGCTCTACCTTTAGAAC 784  
Qy 661 CCTGAAACAAAGAGGAGGAGACATATAGGAATGAGCAGGTACGGCAAGCAAGAGA 720  
Db 785 CTGAAACAAAGAGGAGGAGACATATAGGAATGAGCAGGTACGGCAAGCAAGAGA 844  
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTTGACATTTGATGATGATGATGATGATGATGATGAT 780  
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTCTTTGACATTTGATGATGATGATGATGATGATGATGAT 904  
Qy 781 ATTTAGATTTAAAGTTTGAATGAACAACCTGAAGCAGTCTATTGATAGGAAAGAAATAGC 840  
Db 905 ATTTAGATTTAAAGTTTGAATGAACAACCTGAAGCAGTCTATTGATAGGAAAGAAATAGC 964  
Qy 841 AGTAATTTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTCAGATCAGAG 900  
Db 965 AGTAATTTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTCAGATCAGAG 1024  
Qy 901 ATTCAGATCTGCTGATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 1025 ATTCAGATCTGCTGATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1084  
Qy 961 CAGAATTCCTCAGCCCTCTTTTTCATCACTCTGAATTTTCCAAATATCTGCTGAATAT 1020  
Db 1085 CAGAATTCCTCAGCCCTCTTTTTCATCACTCTGAATTTTCCAAATATCTGCTGAATAT 1144  
Qy 1021 CATATAAATGAAATAATGCTACTCCTGATATAAGAAAGAAAGATGATTAACAATCAGGG 1080  
Db 1145 CATATAAATGAAATAATGCTACTCCTGATATAAGAAAGAAAGATGATTAACAATCAGGG 1204  
Qy 1081 TTCAGTCCACAGAAATTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
Db 1205 TTCAGTCCACAGAAATTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264  
Qy 1141 GCTCAAAATTAAGGGAGACATAGATTTCAATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db 1265 GCTCAAAATTAAGGGAGACATAGATTTCAATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324  
Qy 1201 ATTAGCATCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTTCAGTGGGACTGCTT 1260  
Db 1325 ATTAGCATCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTTCAGTGGGACTGCTT 1384  
Qy 1261 GATTGAAGGAGATGATGAAATCTTATTCCAGGGACCAACATTAACAACCAACCAATCAACA 1320  
Db 1385 GATTGAAGGAGATGATGAAATCTTATTCCAGGGACCAACATTAACAACCAACCAATCAACA 1444  
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361  
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 6  
US-08-483-232-7  
Sequence 7, Application US/08483232  
Patent No. 5656431  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago





100

100

\_\_\_\_\_



RESULT 9  
US-08-910-041-7  
; Sequence 7, Application US/08910041  
; Patent No. 5977308  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,041  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/483,232  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rin-Laures, Li-Hsien  
; REGISTRATION NUMBER: 33,547  
; REFERENCE/DOCKET NUMBER: 27866/34026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 162..1484  
; US-08-910-041-7

Query Match 99.9%; Score 1359.4; DB 2; Length 1520;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TGAGAGACTAGCTGAAGCTGCTCAGCTCCAGAGTGGTGGCCACCCAAATTCATGT 60  
Db 125 TGAGAGACTAAGCTGAAGCTGCTCAGCTCCAGAGTGGTGGCCACCCAAATTCATGT 184  
QY 61 GCATTTCTGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db 185 GCATTTCTGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324

QY 121 TCCGTGTGCCCATATGAATCATCAGCATGGGTCAACAAATACAACTGATGGCTGC 180  
Db 245 TCCGTGTGCCCATATGAATCATCAGCATGGGTCAACAAATACAACTGATGGCTGC 304  
QY 181 TGCAGAGCTTTGGCCAACTAAATCCCGGGGAAATGGCTTATCCGTTGGTGTAC 240  
Db 305 TGCAGAGCTTTGGCCAACTAAATCCCGGGGAAATGGCTTATCCGTTGGTGTAC 364  
QY 241 AGACTTAATGTTTGTATCAGACATAAAGGGCACCTCTTTCGCTTTATATATCCATCCCA 300  
Db 365 AGACTTAATGTTTGTATCAGACATAAAGGGCACCTCTTTCGCTTTATATATCCATCCCA 424  
QY 301 AGATAATGATCGCTTTCACACCTTTTGATCCCAATAAAGAAATATTTTGGGCTCTAG 360  
Db 425 AGATAATGATCGCTTTCACACCTTTTGATCCCAATAAAGAAATATTTTGGGCTCTAG 484  
QY 361 CAAATTTCTTGGACACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAT 420  
Db 485 CAAATTTCTTGGACACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAT 544  
QY 421 GACAACTCTCTGCAAACTGCAATTCCTCTGAGGCTGCTGAAAAATATCCACTTGTGT 480  
Db 545 GACAACTCTCTGCAAACTGCAATTCCTCTGAGGCTGCTGAAAAATATCCACTTGTGT 604  
QY 481 TTTTCTCATGCTTGGGGCACTTTCAGGACACTTTATTTCTCTATTGGCATGACCTGGC 540  
Db 605 TTTTCTCATGCTTGGGGCACTTTCAGGACACTTTATTTCTGCTATTGGCATGACCTGGC 564  
QY 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600  
Db 665 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724  
QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTGAAC 660  
Db 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTGAAC 784  
QY 661 CCTGAACAGAGGAGGAGACACATATACGAATGAGCAGGTACGCGAAAGAGCAAAAGA 720  
Db 785 CCTGAACAGAGGAGGAGACACATATACGAATGAGCAGGTACGCGAAAGAGCAAAAGA 844  
QY 721 ATGTTTCCCAAGCTCTCAGCTGATTTTGATTTGATTTGATTTGATTTGATTTGATTTG 780  
Db 845 ATGTTTCCCAAGCTCTCAGCTGATTTTGATTTGATTTGATTTGATTTGATTTGATTTG 904  
QY 781 ATTAGATTTTAAAGTTTGTATGGAACAACTGAAGCACTTATTGATAGGAAAAAATAGC 840  
Db 905 ATTAGATTTTAAAGTTTGTATGGAACAACTGAAGCACTTATTGATAGGAAAAAATAGC 964  
QY 841 AGTAATTGGACATTTCTTTGGTGGGCAAGCTTATTTCAGACTCTTATGTAAGATCAGAG 900  
Db 965 AGTAATTGGACATTTCTTTGGTGGGCAAGCTTATTTCAGACTCTTATGTAAGATCAGAG 1024  
QY 901 ATTCAGATGTTGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 1025 ATTCAGATGTTGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1084  
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTTCAATATCTGCTAATAT 1020  
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTTCAATATCTGCTAATAT 1144  
QY 1021 CATAAAAATGAAAAATGCTACTCCTGATAAAGAAAGAAAGATGATTTCAATTCAGGGG 1080  
Db 1145 CATAAAAATGAAAAATGCTACTCCTGATAAAGAAAGAAAGATGATTTCAATTCAGGGG 1204  
QY 1081 TTCAAGTCCACAGAAATTTTCTGCTGACTTTCCTTTTGGCAACTGGCAAAATATTTGGACACAT 1140  
Db 1205 TTCAAGTCCACAGAAATTTTCTGCTGACTTTCCTTTTGGCAACTGGCAAAATATTTGGACACAT 1264  
QY 1141 GCTCAAAATTAAGGGAGACATAGATTTCAAAATGAGCTATTGATCTTTAGCAACAAAGCTTC 1200  
Db 1265 GCTCAAAATTAAGGGAGACATAGATTTCAAAATGAGCTATTGATCTTTAGCAACAAAGCTTC 1324  
QY 1201 ATTAGCATTTCTTAAAAAGCATTTAGGACTTCAATAAGATTTTGTGATCAGTGGGACTGCTT 1260

Db 1325 ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384  
Qy 1261 GATTGAAGGAGATGATGAGATCTTTATTCAGGGACCAACATTAACACAAACCAATCAACA 1320  
Db 1385 GATTGAAGGAGATGATGAGATCTTTATTCAGGGACCAACATTAACACAAACCAATCAACA 1444  
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361  
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 10  
US-09-328-474-7  
; Sequence 7, Application US/09328474  
; Patent No. 6045794  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/328,474  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/483,232  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rin-Laures, Li-Hsien  
; REGISTRATION NUMBER: 33,547  
; REFERENCE/DOCKET NUMBER: 27866/34026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 162..1484  
US-09-328-474-7

Query Match 99.9%; Score 1359.4; DB 3; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCCCAACCAATTCATGT 60  
Db 125 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCCCAACCAATTCATGT 184  
Qy 61 GCTTTTCTGCTCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 185 GCTTTTCTGCTCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244  
Qy 121 TCCTGTTGCCCATATGAATCATCAGCATGGTCAACAAATACAAATACAGTACTGATGGCTGC 180  
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGTCAACAAATACAAATACAGTACTGATGGCTGC 304  
Qy 181 TGCAAGCTTTGGCCCAAACTAAAATCCCCCGGGGAAATGGGCTTTATTCGTTGTTGTAC 240  
Db 305 TGCAAGCTTTGGCCCAAACTAAAATCCCCCGGGGAAATGGGCTTTATTCGTTGTTGTAC 364  
Qy 241 ACACCTTAATGTTGATCACACTAATAGGACACCTTCTGCGTTTATATATATCATCCCA 300  
Db 365 AGACCTTAATGTTGATCACACTAATAGGACACCTTCTGCGTTTATATATATCATCCCA 424  
Qy 301 AGATAATGATCGCTTGACACCTTTTGATGCCCAATTAAGAAATATTTTGGGCTCTTAG 360  
Db 425 AGATAATGATCGCTTGACACCTTTTGATGCCCAATTAAGAAATATTTTGGGCTCTTAG 484  
Qy 361 CAAATTTCTTGACACACTGCTTATGCGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 420  
Db 485 CAAATTTCTTGACACACTGCTTATGCGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 544  
Qy 421 GACAACTCCTGCAAACTGGAATCCCTCTCAGGCTGGTGGTGAATAATATCCACTTGTGT 480  
Db 545 GACAACTCCTGCAAACTGGAATCCCTCTCAGGCTGGTGGTGAATAATATCCACTTGTGT 604  
Qy 481 TTTTCTCATGCTGCTTGGGCAATTCAGGACACTTTATCTGCTATTGGCAATTTGACCTGGC 540  
Db 605 TTTTCTCATGCTGCTTGGGCAATTCAGGACACTTTATCTGCTATTGGCAATTTGACCTGGC 664  
Qy 541 ATCTCATGGTTTATAGTTGCTGTAGACACAGATAGATCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 665 ATCTCATGGTTTATAGTTGCTGTAGACACAGATAGATCTGCTGCTGCTGCTGCTGCTGCT 724  
Qy 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGACAACTTTGGGCTTACCTTTAGAAC 660  
Db 725 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGACAACTTTGGGCTTACCTTTAGAAC 784  
Qy 661 CCTGAAACAAGAGGAGGAGACACATATACGAATAGCAGGACGCGCAAGAGCAAAAGA 720  
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAATAGCAGGACGCGCAAGAGCAAAAGA 844  
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTCATCATGGAAGCCAGTGAAGAATGC 780  
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTCATCATGGAAGCCAGTGAAGAATGC 904  
Qy 781 ATTAGATTTAAAGTTTGTATGGAACACTGAAGACTCTTATTGATAGGGAATAATAGC 840  
Db 905 ATTAGATTTAAAGTTTGTATGGAACACTGAAGACTCTTATTGATAGGGAATAATAGC 964  
Qy 841 AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAG 900  
Db 965 AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAG 1024  
Qy 901 ATTACAGATGTTGTTATGCGCTGGATGCTGATTTTCCACTGGCTGATGAAGTATATTC 960  
Db 1025 ATTACAGATGTTGTTATGCGCTGGATGCTGATTTTCCACTGGCTGATGAAGTATATTC 1084  
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATTCCTGCTTAATAT 1020  
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATTCCTGCTTAATAT 1144  
Qy 1021 CATAAAAATGAAAAAATGCTACTCACCTGATGAAGAGCAAGATGATTACAAATCAGGGG 1080



Qy	901	ATT	CAGATGTGCTATTGGCCCTGGATGCATGATCTTTCCACTGGGTGATGAATATATTC	960
Db	1025	ATT	CAGATGTGCTATTGGCCCTGGATGCATGATGCTTTCCACTGGGTGATGAAGTATATTC	1084
Qy	961	CAGA	ATTCCTGAGCCCTCTTTTATCAACACTCTGAATATTTTCCAATATCCTGCTAAATAT	1020
Db	1085	CAGAA	TCTCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCCCTGCTAATAT	1144
Qy	1021	CATAAAAATG	AAAAATGCTACTCACTCTGATAAAGAAAGAAAGATGATTAACAATCAGGGG	1080
Db	1145	CATAAAAATG	AAAAATGCTACTCACTCTGATAAAGAAAGAAAGATGATTAACAATCAGGGG	1204
Qy	1081	TT	CAGTCCACGAGAATTTTGCTGACTTCACCTTTTGGCACTCGGCAAAATAATTCGACACAT	1140
Db	1205	TT	CAGTCCACGAGAATTTTGCTGACTTCACCTTTTGGCACTCGGCAAAATAATTCGACACAT	1264
Qy	1141	GCT	CAAAATTAAGGGAGACATAGATTCAAAATCGACGTATTGATCTTAGCAACAAGAGCTTC	1200
Db	1265	GC	TCAAAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACAAGAGCTTC	1324
Qy	1201	ATT	PAGCATCTTTACAAAAGCATTTTAGCACTTCATAAAGATTTTGATCAGTGGGACTGCTTT	1260
Db	1325	ATT	AGCATTTCTTACAAAAGCATTTTAGCACTTCATAAAGATTTTGATCAGTGGGACTGCTTT	1384
Qy	1261	GATT	GAAGGAGATGATGAGAATCTTATTCCAGGGGACCAACATTAACACAACTCAATCAACA	1320
Db	1385	GATT	GAAGGAGATGATGAGAATCTTATTCCAGGGGACCAACATTAACACAACTCAATCAACA	1444
Qy	1321	CAT	CATGTTACAGAACTCTTTCAGGAANTAGAGAAATACAAATTT	1361
Db	1445	CAT	CATGTTACAGAACTCTTTCAGGAANTAGAGAAATACAAATTT	1485

RESULT 12

364	TGCAAGCTTTGGCCAAACTAAATAATCCCGGGGAAATGGCCCTTATTCGGTTGGTGTAC	Db
305		
241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTCTCTGGCTTATATATATCCCATCCCA	Qy
365	AGACTTAATGTTTGATCACACTAATAAGGGCACCTCTCTGGCTTATATATATCCCATCCCA	Db
301	AGATAATGATCGCCTTGACACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG	Qy
425	AGATAATGATCGCCTTGACACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG	Db
361	CAAAATTTCTTGGAAACACACATGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT	Qy
485	CAAAATTTCTTGGAAACACACATGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT	Db
421	GACAACTCCTGCAAACTGGAAATCCCCCTCTGAGGCGCTGGTGAAAAATATATCCACTTGTGT	Qy
545	GACAACTCCTGCAAACTGGAAATCCCCCTCTGAGGCGCTGGTGAAAAATATATCCACTTGTGT	Db
481	TTTTTCTCATGCTCTGGGGCATTCAGGACACCTTTATTTCTGCTATTGGCATTTGACCTGGC	Qy
605	TTTTTCTCATGCTCTGGGGCATTCAGGACACCTTTATTTCTGCTATTGGCATTTGACCTGGC	Db
541	ATCTCATATGGGTTTATAGTTGCTGTGTAGAACACAGAGATATGATATCGCATCTGCAACTTA	Qy
665	ATCTCATATGGGTTTATAGTTGCTGTGTAGAACACAGAGATATGATATCGCATCTGCAACTTA	Db
601	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTTGGCTCTTACTCTTAGAAC	Qy
725	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTTGGCTCTTACTCTTAGAAC	Db
661	CCTGAAACAAGAGGAGGAGACACATATACGAAATGACAGGTTACGGCAAGAGCAAAAGA	Qy
785	CCTGAAACAAGAGGAGGAGACACATATACGAAATGACAGGTTACGGCAAGAGCAAAAGA	Db
721	ATGTTGCCCAAGCTCTCAGTCTGATTCTTTGACATTTGATATGAAAGCCAGTGAAGAATGC	Qy
845	ATGTTGCCCAAGCTCTCAGTCTGATTCTTTGACATTTGATATGAAAGCCAGTGAAGAATGC	Db



QY 781 ATTAGATTAAAGTTTGATATGGAACAACCTGAGGACTCTATTGATAGGGAAAAATAGC 840  
Db 905 ATTAGATTAAAGTTTGATATGGAACAACCTGAGGACTCTATTGATAGGGAAAAATAGC 964  
QY 841 AGTAATTGACATCTCTTTGGTGGAGCAACGCTTATTGAGACTCTTTAGTGAAGATCAGAG 900  
Db 965 AGTAATTGACATCTCTTTGGTGGAGCAACGCTTATTGAGACTCTTTAGTGAAGATCAGAG 1024  
QY 901 ATTACAGATGCTGATTGGCTCGATGATGATGCTTCCACTGGGTGATGAACTATATTC 960  
Db 1025 ATTACAGATGCTGATTGGCTCGATGATGATGCTTCCACTGGGTGATGAACTATATTC 1084  
QY 961 CAGAAATCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCGCTAATAT 1020  
Db 1085 CAGAAATCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCGCTAATAT 1144  
QY 1021 CATAAAATGAAAAATGCTACTCACTGATAAAGAGAAAGATGATTAACAATCAGGG 1080  
Db 1145 CATAAAATGAAAAATGCTACTCACTGATAAAGAGAAAGATGATTAACAATCAGGG 1204  
QY 1081 TTCAGTCCACCAAGATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGACACAT 1140  
Db 1205 TTCAGTCCACCAAGATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGACACAT 1264  
QY 1141 GCTCAATTAAGGAGACATAGATTCAATGCAAGCTATTGATCTTAGCAACAAGCTTC 1200  
Db 1265 GCTCAATTAAGGAGACATAGATTCAATGCAAGCTATTGATCTTAGCAACAAGCTTC 1324  
QY 1201 ATTACATCTTACAAAAGCATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1260  
Db 1325 ATTACATCTTACAAAAGCATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1384  
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACAACCAATCAACA 1320  
Db 1385 GATTGAAGGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACAACCAATCAACA 1444  
QY 1321 CATCATGTTACAGACTCTTCAGGAATAGAGAAATACAAT 1361  
Db 1445 CATCATGTTACAGACTCTTCAGGAATAGAGAAATACAAT 1485

## RESULT 13

US-09-577-758-7  
; Sequence 7, Application US/09577758  
; Patent No. 6203790  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/577,758  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/010,715

; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6203790and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32793  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 162..1484  
; US-09-577-758-7

Query Match 99.9%; Score 1359.4; DB 4; Length 1520;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TGAGAGACTAAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCCAATTCATGT 60  
Db 125 TGAGAGACTAAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCCAATTCATGT 184  
QY 61 GCTTTTCGCTCTCGGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120  
Db 185 GCTTTTCGCTCTCGGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 244  
QY 121 TCCTGTTGCCCATATCAATCATCAGCATGGTCAACAAAATACAAAGTACTGATGGCTGC 180  
Db 245 TCCTGTTGCCCATATCAATCATCAGCATGGTCAACAAAATACAAAGTACTGATGGCTGC 304  
QY 181 TCGAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCTGGTGGTGTGAC 240  
Db 305 TCGAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCTGGTGGTGTGAC 364  
QY 241 AGACTTAATGTTTGTATCAGTCACTAATAAGGGCACCTTCTTGGCTTTATATTTATCATCCCA 300  
Db 365 AGACTTAATGTTTGTATCAGTCACTAATAAGGGCACCTTCTTGGCTTTATATTTATCATCCCA 424  
QY 301 AGATAATGATGCTTGCACACCTTTGGATCCCAAAATAAAGAAATATTTTGGGCTCTTAG 360  
Db 425 AGATAATGATGCTTGCACACCTTTGGATCCCAAAATAAAGAAATATTTTGGGCTCTTAG 484  
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGTTCAAT 420  
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGTTCAAT 544  
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RESULT 14
US-08-483-232-30
; Sequence 30, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-483-232-30

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Query Match 85.4%; Score 1162.4; DB 1: Length 1335;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Db 61 CCTTTTACTGGCAATACATAAATCCTGTTGCCCATATGAATCATCATGATGGTCAAC 120
QY 158 AAAATACAAAGTACTGATGCTGCTGCAAGCTTTGGCCAAACTTAAATCCCGGGGAAAT 217
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QY 218 GGGCTTATTCCTGTTGGTGTACAGACTTAAATGTTGATCAGACTTAATAAGGACCTTC 277
Db 181 GGGCTTATTCCTGTTGGTGTACAGACTTAAATGTTGATCAGACTTAATAAGGACCTTC 240
QY 278 TTGGTATTATATTCATCCCAAGATAATGATCGCTTTGACACCCCTTTGGATCCCAAT 337
Db 241 CTGAGACTGTACTACCCGACGAGGACCAAGACAGACTGGATACTCTGTGGATCCCAAT 300
QY 338 AAGAATATTTTGGGTCTTAGCAATTTCTTGAACACACTGCTTATGGGAACAT 397
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COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,938A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5847088and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32792  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-485-938A-30

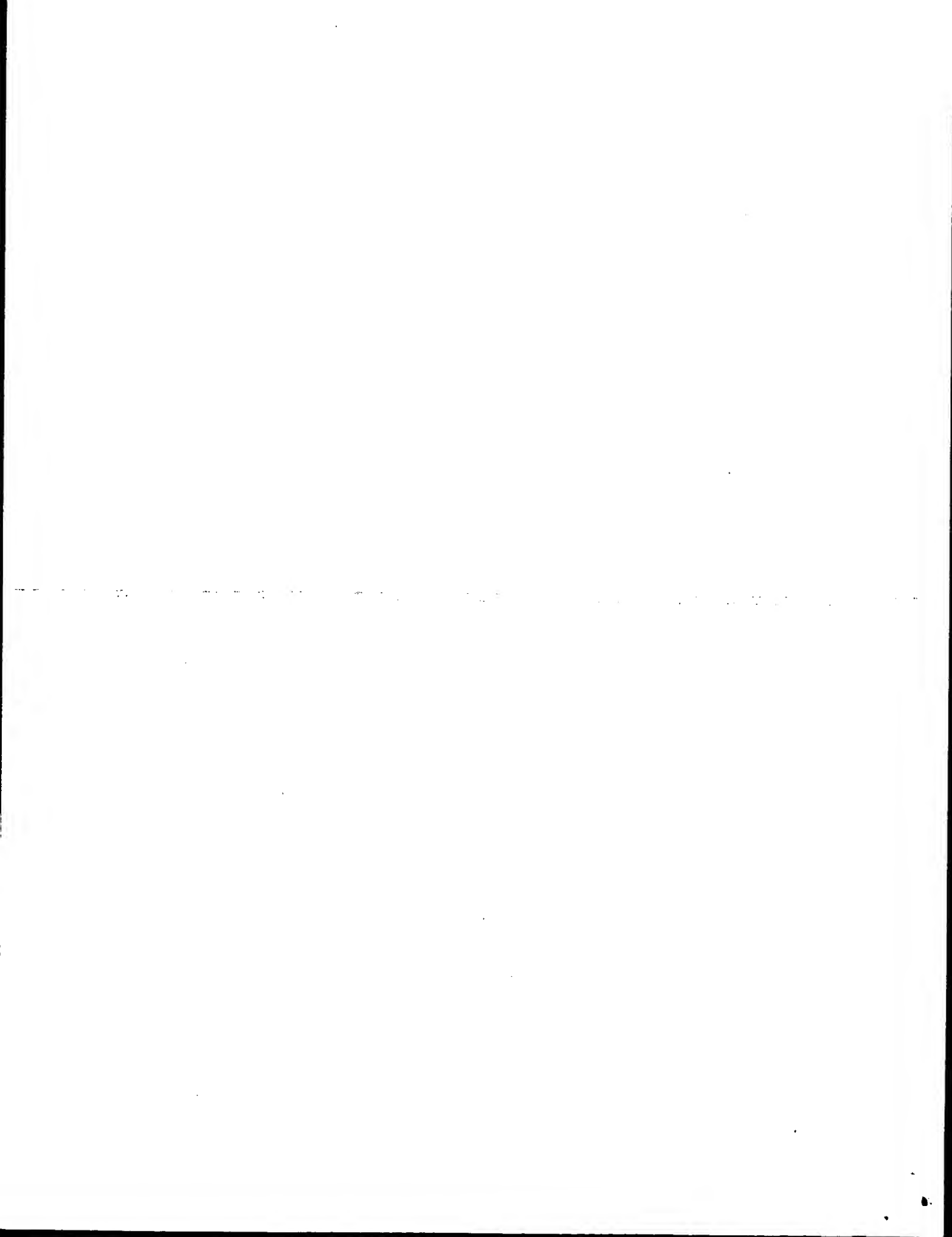
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Query Match      85.4%; Score 1162.4; DB 2; Length 1335;
Best Local Similarity 92.4%; Pred. NO. 0;
Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
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RESULT 15  
 US-08-485-938A-30  
 : Sequence 30, Application US/08485938A  
 : Patent No. 5847088  
 : GENERAL INFORMATION:  
 : APPLICANT: Cousins, Lawrence S.  
 : APPLICANT: Eberhardt, Christine D.  
 : APPLICANT: Gray, Patrick W.  
 : APPLICANT: Le Trong, Hai  
 : APPLICANT: Tjoelker, Larry L.  
 : APPLICANT: Wilder, Cheryl L.  
 : TITLE OF INVENTION: Platelet-Activating Factor  
 : TITLE OF INVENTION: Acetylhydrolase  
 : NUMBER OF SEQUENCES: 36  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 : STREET: 6300 Sears Tower, 233 South Wacker Drive  
 : CITY: Chicago  
 : STATE: Illinois

181	GGCCCTACAGCGTGGCTGCACCGATCTGATGTTGCACATACCAACAAAGGAACATTTT	240
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421	GGTGAATAATATCCACTGTTGTTTTTCTCATGGTCTTTGGGGCAATTCAAGACACTTTAT	480
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Search completed: March 8, 2002, 23:05:20  
 Job time: 3863 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:47:12 ; Search time 1552.89 seconds  
(without alignments)  
9417.927 Million cell updates/sec

Title: US-09-922-067-9

Perfect score: 1361

Sequence: 1 TCAGAGACTAGCTGAACT.....AGGAATAGAGAAATACAAAT 1361

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estfun:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estom:\*
- 5: em\_estpi:\*
- 6: em\_estba:\*
- 7: em\_estro:\*
- 8: em\_estov:\*
- 9: em\_hic:\*
- 10: gb\_est1:\*
- 11: gb\_est2:\*
- 12: gb\_hic:\*
- 13: gb\_gss:\*
- 14: em\_gss\_fun:\*
- 15: em\_gss\_hum:\*
- 16: em\_gss\_inv:\*
- 17: em\_gss\_pln:\*
- 18: em\_gss\_pro:\*
- 19: em\_gss\_rod:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	912.6	67.1	932	10	AL575852
c 2	844.6	62.8	978	10	AL554852
c 3	822.2	60.4	875	10	AL573565
c 4	785.2	57.7	1695	12	AK005210
c 5	758.6	55.7	991	10	AL552617
c 6	716	52.6	893	10	AL549288
c 7	643.6	47.3	1376	12	AK005158
c 8	590.2	43.4	900	11	BG530083
c 9	571.2	42.0	650	10	AI343491
c 10	529.6	38.9	874	11	BI182205
c 11	513.6	37.7	598	11	BF509203
c 12	497.4	36.5	519	10	AW071677

c 13	483.8	35.5	560	11	BF508812
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c 15	420	30.9	851	11	BG918925
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c 19	379.2	27.9	928	11	BG519457
c 20	372.4	27.4	827	11	BG921765
c 21	370	27.2	394	10	AI770111
c 22	364.8	26.8	816	10	AU080891
c 23	359.8	26.4	541	10	AW321503
c 24	356.4	26.2	663	10	AA183265
c 25	353.6	26.0	453	10	AW461498
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c 29	331.4	24.3	828	11	BG917419
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c 36	304.4	22.4	727	11	BF168295
c 37	304	22.3	720	10	AU067449
c 38	302.8	22.2	379	10	AA297235
c 39	302.4	22.2	537	10	BE281780
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prime, mRNA sequence.  
EST  
AL575852.1 GI:12937422  
EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 932)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
FEATURES  
Location/Qualifiers  
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/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

BASE COUNT 255 a 190 c 181 g 299 t 7 others  
ORIGIN

Query Match 67.1%; Score 912.6; DB 10; Length 932;  
Best Local Similarity 98.2%; Pred. No. 6.2e-218;  
Matches 915; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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Db 32 ATCATGTTTACAGAACTCTTCCAGGAATAGAGAA 1

RESULT 2  
AL554852

LOCUS

DEFINITION

AL554852 LTI\_NFL006\_PL2 Homo sapiens

ACCESSION

AL554852

VERSION

AL554852.1

KEYWORDS

EST.

SOURCE

ORGANISM

1 (bases 1 to 978)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..978

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was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with NotI and

cloned into the NotI and EcoRV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 253 a 216 c 237 g 270 t 2 others

ORIGIN

Query Match 62.8%; Score 854.6; DB 10; Length 978;

Best Local Similarity 99.3%; Pred. No. 2.1e-203;

Matches 857; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCATGT 60

Db 116 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCATGT 175

QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 176 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235

QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGCTCAACAAATACAAAGTACTGATGGCTGC 180

Db 236 TCCTGTTGCCCATATGAATCATCAGCATGGCTCAACAAATACAAAGTACTGATGGCTGC 295

QY 181 TCACAGCTTTGGCCAACTAAATCCCGGGGAAATGGCGTTTATTCCTGTTGGTTGTAC 240

Db 296 TCACAGCTTTGGCCAACTAAATCCCGGGGAAATGGCGTTTATTCCTGTTGGTTGTAC 355

QY 241 AGACCTAATGTTTGTATCATCAGCTTAATAAGGCGACCTCTTCTGCTTTATATTTATTCATCCCA 300

Db 356 AGACCTAATGTTTGTATCATCAGCTTAATAAGGCGACCTCTTCTGCTTTATATTTATTCATCCCA 415

QY 301 ACATATATCATCCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360

Db 416 ACATATATCATCCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 475

QY 361 CAAATTTCTTGGAAACACACTGGCTTTATGGGCAACATTTTGGAGTTTACTCTTTGGTTCAAT 420

Db 476 CAAATTTCTTGGAAACACACTGGCTTATATGGCAACATTTTCAGGTTACTCTTTGGTTCAAT 535  
Qy 421 GACAACTCCTCAAACTGGAAATTCCTCTCAGCCCTGGTGAANAATATCCACTTCTTGT 480  
Db 536 GACAACTCCTCAAACTGGAAATTCCTCTCAGCCCTGGTGAANAATATCCACTTGTGT 595  
Qy 481 TTTTCTCATGGTCTTGGGGATTCAGGACACTTTATCTGCTATTGGCAATTCACCTGGC 540  
Db 596 TTTTCTCATGGTCTTGGGGATTCAGGACACTTTATCTGCTATTGGCAATTCACCTGGC 655  
Qy 541 ATCTCATGGGTTTATAGTCTGCTGTAGAACACAGAGATAGATCTGCACTCTCAACTTA 600  
Db 656 ATCTCATGGGTTTATAGTCTGCTGTAGAACACAGAGATAGATCTGCACTCTCAACTTA 715  
Qy 601 CTATTTCAAGACCAATCTGCTGCAGAAATAGGGGACAGCTCTTGGCTCTACCTTAGAAC 660  
Db 716 CTATTTCAAGACCAATCTGCTGCAGAAATAGGGGACAGCTCTTGGCTCTACCTTAGAAC 775  
Qy 661 CCTGAACAAGAGAGAGACACATATACGAATAGAGAGCTACGGCAAGAGACAAAGA 720  
Db 776 CCTGAACAAGAGAGAGACACATATACGAATAGAGAGCTACGGCAAGAGACAAAGA 835  
Qy 721 ATGTTCCCAAGCTCTAGTCTGATCTTGACATTGATCATGGAAGCCAGTGAAGATGC 780  
Db 836 ATGTTCCCAAGCTCTAGTCTGATCTTGACATTGATCATGGAAGCCAGTGAAGATGC 840  
Qy 781 ATTAGATTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGCAAAATAGC 895  
Db 896 ATTAGATTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGCAAAATAGC 955  
Qy 841 AGTAATTTGGACATCTTTTGGTG 863  
Db 956 AGTCATTTGGACATCTTTTGGTG 978

RESULT 3  
AL573565/c  
LOCUS  
DEFINITION AL573565 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS001049YE02 3  
ACCESION AL573565  
VERSION AL573565.1 GI:12932922  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 875)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1. 875  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="LTI\_NFL006\_PL2"  
/tissue\_type="Placenta"  
/note="Vector: PCWSPORT 6; Site\_1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the PCWSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
227 a 187 c 166 g 263 t 32 others

BASE COUNT

## ORIGIN

Query Match 60.4%; Score 822.2; DB 10; Length 875;  
Best Local Similarity 94.3%; Pred. No. 2.6e-195;  
Matches 825; Conservative 23; Mismatches 27; Indels 0; Gaps 0;  
Qy 431 GC AAAAATGGAATTCCTCTCTGAGGCTGTGTA AAAAATATCCACTTGTGTGTTCATCAT 490  
Db 875 GC AAAAATGGAATTCCTCTCTGAGGCTGTGTA AAAAATATCCACTTGTGTGTTCATCAT 816  
Qy 491 GGTCTTGGGGATTCAGGACACTTTTATTCGTATTGGCATTTGACCTGGCATCTCATGGG 550  
Db 815 GGTCTTGGGGATTCAGGACACTTTTATTCGTATTGGCATTTGACCTGGCATCTCATGGG 756  
Qy 551 TTTATAGTTGCTGCTGTAGAACACAGATAGATCTGCATCTGCAACTTACTATTTCAGG 610  
Db 755 TTTATAGTTGCTGCTGTAGAACACAGATAGATCTGCATCTGCAACTTACTATTTCAGG 696  
Qy 611 GACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTTAGAACCTCGAACAA 670  
Db 695 GACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTTAGAACCTCGAACAA 636  
Qy 671 GAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAA 730  
Db 635 GAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAA 576  
Qy 731 GCTCTCAGTCTGATTTCTTGACATTTGATCATGCAAGGACAGTGAAGAATGCATTTAGATTA 790  
Db 575 GCTCTCAGTCTGATTTCTTGACATTTGATCATGCAAGGACAGTGAAGAATGCATTTAGATTA 516  
Qy 791 AAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGCAAAATAGCAGTAAATTCGA 850  
Db 515 AAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGCAAAATAGCAGTAAATTCGA 456  
Qy 851 CATTCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGT 910  
Db 455 CAGTCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGT 396  
Qy 911 GGTATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970  
Db 395 GGTATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 336  
Qy 971 CAGCCCTCTTTTATCACTCTGCAATATTTCCCAATATCTGCTAATATCATATCAATCAATG 1030  
Db 335 CAGCCCTCTTTTATCACTCTGCAATATTTCCCAATATCTGCTAATATCATATCAATCAATG 276  
Qy 1031 AAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGGTTTCACTCCAC 1090  
Db 275 MAAAATGCMACCTCMCTGTATAAGAAAGAAAGATGATSACAATCAGGGGCTCAGCCMC 216  
Qy 1091 CAGATTTTGTGACTTCACTTTTGGCAACTGGCAAAATATTTGGACACATGCTCAATTA 1150  
Db 215 CAGATTTTGTGACTTCACTTTTGGCAACTGGCAAAAGAAATTTGGACACATGCTCAATTA 156  
Qy 1151 AAGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCAATAGCATTC 1210  
Db 155 AAGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCAATAGCATTC 96  
Qy 1211 TTACAAAGCATTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTCTTGTGATGAAGGA 1270  
Db 95 TTWTAATTCATTTAGGACHCTCAATAATGATTTTGTGATCAGTGGGACTCTTGTGATGAAGGA 36

## RESULT 4

AK005210  
LOCUS  
DEFINITION AK005210 1695 bp mRNA  
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched  
library, clone:1500011H20, full insert sequence.  
05-JUL-2001  
HTC











JOURNAL COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CMI524 row: e column: 12  
High quality sequence stop: 628.  
Location/Qualifiers  
1. 900  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4696691"  
/clone\_lib="NIH\_MGC\_61"  
/tissue\_type="embryonal carcinoma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: testis; Vector: pDR-LIB (Clontech); Site\_1: SfiI (ggccgctggccc); Site\_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

FEATURES source

BASE COUNT 305 a 144 c 215 g 236 t  
ORIGIN  
Query Match 43.4%; Score 590.2; DB 11; Length 900;  
Best Local Similarity 98.0%; Pred. No. 3.1e-137;  
Matches 630; Conservative 0; Mismatches 8; Indels 5; Gaps 3;  
Qy 670 AGAGGAGGAGACATATACGAATGAGCAGGTACGCAAGAGCAAGAAAGATGTTCCCA 729  
Db 1 AGAGGAGGAGACATATACGAATGAGCAGGTACGCAAGAGCAAGAAAGATGTTCCCA 60  
Qy 730 AGCTCTCAGTGTGATCTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 789  
Db 61 AGCTCTCAGTGTGATCTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
Qy 790 AAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATGAGGAAAAAATAGCAGTAATTCG 849  
Db 121 AAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATGAGGAAAAAATAGCAGTAATTCG 180  
Qy 850 ACATTCCTTTGGTGGACACGGTATTACAGACTCTAGTGAAGATCAGAGATTCAGATG 909  
Db 181 ACATTCCTTTGGTGGACACGGTATTACAGACTCTAGTGAAGATCAGAGATTCAGATG 240  
Qy 910 TGGTATTCCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 969  
Db 241 TGGTATTCCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
Qy 970 TCAGCCCTCTTTTATCAACCTCAATATTTCCAAATCTGCTCAATATCATATAAAT 1029  
Db 301 TCAGCCCTCTTTTATCAACCTCAATATTTCCAAATCTGCTCAATATCATATAAAT 360  
Qy 1030 GAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTCAAGTCA 1089  
Db 361 GAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTCAAGTCA 420  
Qy 1090 CCAGAAATTTTGGCTGACTTCACTTTTCCAACTGCAAAATTAATGGACATGCTCAAA-- 1147  
Db 421 CCAGAAATTTTGGCTGACTTCACTTTTCCAACTGCAAAATTAATGGACATGCTCAAAAT 480  
Qy 1148 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 1207

Db 481 TAACAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 540  
Qy 1208 TTCTTACAAAGCAATTTAGGACTTTCATAAAGATTTTGTATGATGGGACTGCTGATTGAA 1267  
Db 541 TTCTTACAAAGCAATTTAGGACTTTCATAAAG--TTGATCAGTGGGACTGCTGATTGAA 598  
Qy 1268 GG-AGATGATGAGATCTTTATTCAGGACCAACATTTAACACA 1309  
Db 599 GGCAGATGATGAGATCTTTATTCAGGACCAACATTTAACACA 641  
RESULT 9  
AI343491/c 650 bp mRNA EST 08-APR-1999  
LOCUS tb97c04.x1 NCI-CGAP\_Col6 Homo sapiens cDNA clone IMAGE:2062278 3'  
DEFINITION similar to SW:PAPA.HUMAN Q13093 PLATELET-ACTIVATING FACTOR  
ACETYLHYDROLASE PRECURSOR ;, mRNA sequence.  
ACCESSION AI343491 GI:4080697  
VERSION EST.  
KEYWORDS  
SOURCE Homo Sapiens  
ORGANISM  
REFERENCE 1 (bases 1 to 650)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgaf.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 785 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 439.  
Location/Qualifiers  
1. 650  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2062278"  
/clone\_lib="NCI-CGAP\_Col6"  
/tissue\_type="colon tumor, RER+"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP\_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 186 a 123 c 107 g 233 t  
ORIGIN  
Query Match 42.0%; Score 571.2; DB 10; Length 650;  
Best Local Similarity 98.7%; Pred. No. 1.8e-132;  
Matches 607; Conservative 0; Mismatches 4; Indels 4; Gaps 3;  
Qy 751 CATTGATCATCGAAGCAGTGAA--CAATGCAATTAGATTAA--GTTTGATATGAA-C 806  
Db 645 CATTGATCAAGGAAGCAGTGAAAGAAATGCTTTAGATTAAAGGTTTGTATGGAAC 586  
Qy 807 AACTGAAGGACTCTATTGATAGGAAAAAATAGCAGTAATTGGACATTCCTTTGGTGAG 866

[illegible]



/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"

/note="Organ; brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGGCATAGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 150 a 95 c 93 g 181 t

ORIGIN

Query Match 36.5%; Score 497.4; DB 10; Length 519;

Best Local Similarity 99.8%; Pred. No. 5.2e-114;

Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 CGAGCAACGGTTATTCACACTCTTAGTGAAGATCAGAGATTCAGATGGTATGGCCCTG 922

Db 519 GGAGCAACGGTTATTCACACTCTTAGTGAAGATCAGAGATTCAGATGGTATGGCCCTG 460

QY 923 GATGATGATGTTTCCACTGGGTGATGAAGTATATCCAGAAATTCCTCAGCCCTCTTT 982

Db 459 GATGATGATGTTTCCACTGGGTGATGAAGTATATCCAGAAATTCCTCAGCCCTCTTT 400

QY 983 TTTATCAACTCTGATATTTCCATATCTCTGCTATATCATATAAAATGAAATGCTAC 1042

Db 399 TTTATCAACTCTGATATTTCCATATCTCTGCTATATCATATAAAATGAAATGCTAC 340

QY 1043 TCACCTGATAAGAAAGAGATGATTACAATCAGGGGTTCCAGTCCACCAAGATTTTGGCT 1102

Db 339 TCACCTGATAAGAAAGAGATGATTACAATCAGGGGTTCCAGTCCACCAAGATTTTGGCT 280

QY 1103 GACTTCACCTTTGCAACTGGCAATATATTCGACACATGCTCAAAATTAAGGGAGACATA 1162

Db 279 GACTTCACCTTTGCAACGAGCAAAATATTTGGACACATGCTCAAAATTAAGGGAGACATA 220

QY 1163 GATTCAAAATGACGCTATTGATCTTAGCAACAAAGCTTCATTAGCATCTTACAAAAGCAT 1222

Db 219 GATTCAAAATGACGCTATTGATCTTAGCAACAAAGCTTCATTAGCATCTTACAAAAGCAT 160

QY 1223 TTAGGACTTCATAGATTTTGATCAGTGGGACTGCTTGATTTGAGGAGATGAGAAAT 1282

Db 159 TTAGGACTTCATAGATTTTGATCAGTGGGACTGCTTGATTTGAGGAGATGAGAAAT 100

QY 1283 CTTATCCAGGACCAACATTAACACACCAATCAACACATCATGTTACAGAACTCTTCA 1342

Db 99 CTTATCCAGGACCAACATTAACACACCAATCAACACATCATGTTACAGAACTCTTCA 40

QY 1343 GGAATAGAGAAATACAAAT 1361

Db 39 GGAATAGAGAAATACAAAT 21

RESULT 13

BF508812/c

LOCUS 560 bp mRNA EST 06-DEC-2000

DEFINITION UI-H-B14-aor-b-03-0-UI.sl NCI\_CGAP\_Sub8 Homo sapiens cDNA clone

IMAGE:3085757 3', mRNA sequence.

ACCESSION BF508812

VERSION BF508812.1 GI:11592110

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

POLYA=Yes

Location/Qualifiers

1..560

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3085757"

/clone\_lib="NCI\_CGAP\_Sub8"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; NCI\_CGAP\_Sub8

is a subtracted library derived from NCI\_CGAP\_Sub5. The

NCI\_CGAP\_Sub8 library had 2.5 million recombinants. A

single-stranded DNA preparation of NCI\_CGAP\_Sub5 was used

as a tracer in a subtractive hybridization with a driver

clone Ids 2732833-2737415, 3068040-3069191; 25% of the

driver population), a pool of clones from NCI\_CGAP\_Sub4

(IMAGE clone Ids 2725592-2729326; 25% of the driver

population), NCI\_CGAP\_Sub6 (pool AIF-AJU, IMAGE Ids

2728969-2733190; 25% of the driver population), and

NCI\_CGAP\_Sub7 (IMAGE Ids 3069192-3072238, 3081864-3084550

; 25% of the driver population). Subtraction was

performed as previously described (Bonaldo, Lennon &

Soares (1996): Normalization and Subtraction: Two

Approaches To Facilitate Gene Discovery. Genome Research

6, 791-806.

TAG\_LIB=NCI\_CGAP\_Leid2

TAG\_TISSUE=leiomyosarcoma

TAG\_SEQ=AATCG"

BASE COUNT 160 a 99 g 204 t

ORIGIN

Query Match

Best Local Similarity 96.6%; Pred. No. 1.3e-110;

Matches 505; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 840 CAGTAATTCGACATCTTTTGGTGGAGCAACGCTTATTTCAGACTCTTACTGAAGATCAGA 899

Db 560 CAGTAATTCGACATCTTTTGGTGGAGCAACGCTTATTTCAGACTCTTACTGAAGATCAGA 501

QY 900 GATTTCAGATGTGTTATTCGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATT 959

Db 500 GATTTCAGATGTGTTATTCGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATT 441

QY 960 CCAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTGAATA 1019

Db 440 CCAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTGAATA 381

QY 1020 TCATAAAATGAAAATGCTACTACCTGATAAGAAAGAAAGATGATTACATCAGG 1079

Db 380 TCATAAAATGAAAATGCTACTACCTGATAAGAAAGAAAGATGATTACATCAGG 321

QY 1080 GTTCAGTCCACCAAGAAATTTTGTGCTTACCTTTTCCAACTGGCAAAATTAATTTGGACAC- 1138

Db 320 GTTCAGTCCACCAAGAAATTTTGTGCTTACCTTTTCCAACTGGCAAAATTAATTTGGACACG 261

QY 1139 ATGCTCAAAATTAAGGGAGACATAGATTCAATGACGCTATTGATCTTAGCAACAAGCT 1198

Db 260 ATGCTCAAAATTAAGGGAGACATAGATTCAATGACGCTATTGATCTTAGCAACAAGCT 201

QY 1199 TCATTAGCATCTTTACAAAAGCATTTAGCACTTCATAAAGATTTTTCAGTGGGACCTGTC 1258

Db 1199 TCATTAGCATCTTTACAAAAGCATTTAGCACTTCATAAAGATTTTTCAGTGGGACCTGTC 1258







Search completed: March 8, 2002, 23:02:59  
Job time: 4547 sec

/clone="IMAGE:4948378"  
/clone\_lib="NCI\_CGAP\_Mam6"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT		225 a	193 c	205 g	228 t		
ORIGIN							
Query Match		30.9%	Score 420;	DB 11;	Length 851;		
Best Local Similarity		73.7%	Pred. No. 1.2e-94;				
Matches 615;		Conservative	0;	Mismatches 210;	Indels	9;	Gaps 6;
QY	5	AGACTAAGCTGAACCTGCTCAGCTCCAGATGGTGGCCACCAAAATGCAATGCTT	64				
Db	24	ACATCAAACTGAAGCCACTGCTCAGCTCCTAAGATGGTACCACTCAAACTGCAGCGCTT	83				
QY	65	TTTCTGCCCTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	124				
Db	84	TTTCTGCCCTCTGCTGCTGCCATCCATGCTTCTACTGGCAAGACACATCTCT	143				
QY	125	GTTCGCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGCTGCA	184				
Db	144	TTTG---ACTTCAGGCGCTCAGTAATGTTTCAACAGCTCCAAATCGGTGATGCTGCTGCC	200				
QY	185	AGCTTTGGCCAACTAAATCCCGGGGAATGGGCTTATTCGGTTGGTTGTACAGAC	244				
Db	201	GGCTCTGGCCATAGTAAATCCCAAGGAATGGATCCACCCCGCTGGTTGTACAGAT	260				
QY	245	TTAATGTTTGTATGATCAGCTAATAAGGCGCTTCTTCGCTTATATATATCCATCCCAAGAT	304				
Db	261	CTGATGTTTCGGTTATGGGAATGAGAGCGTCTTCGTGCTTGTACTACCCAGCTCAAGAT	320				
QY	305	AATGATGCTTTCACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTTAGCAAA	364				
Db	321	CAAGTGGCTCGACACTGTTTGGATCCCAACAAAGAAATATTTTGGGCTCTTAGTATA	380				
QY	365	TTTCTTGGAAACACACTGGCTTATGGCAACATTTTGAAGTACTCTTTGGTTCAATGACA	424				
Db	381	TTTCTTGGAAACACCCAGTATTTAGGCAATATTTTACACTCTTATATGTTCTCTGACA	440				
QY	425	ACTCTGCAAACTGGAATTCCTCTGAGCGCTGGTGAATAATTCACACTTGTGTTTTT	484				
Db	441	ACTCTGCAAGCTGGAATTCCTTTGAGGACTGGAGAAAAATACCCGCTCATTTGCTTT	500				
QY	485	TCTCATGCTCTTGGGGATTCAGGACACTTTTCTGCTATTTGGCATTTGACCTGGCACT	544				
Db	501	TCTCATGCTCTCGAGCCTTCAGGACGATTTATTCGCTATTTGGCATTTGGCCTGGCATCT	560				
QY	545	CATGGGTTTATAGTCTGCTGCTGAGAACACAGATAGATCTGCATCTGCACTTACTAT	604				
Db	561	AATCGGTTTATAGTGGACACTGTCGAACACAGACAGATCTGCATCGGCAACTTACTTT	620				
QY	605	TTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGCTTTCGCTCTACCTTTAGAACCTTG	664				
Db	621	TTGAA-GACCAGTGGCTGCAAGTGGAAACAGGCTTTCGCTTTTACCTGAGAAAAGTC	679				
QY	665	AAACAAGAGGAG-GAGACACATATACGAATGAGCAGGTACGGCAAGCAAGCAAGATG	723				
Db	680	AAACAAGAGGAGTGGACAGTGTCCGGAACAGCAAGCAAGTTCAGCAAGAGCAGTAAATG	739				
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OM of: US-09-922-067-9 to: A\_Geneseq\_1101.\* out\_format : pfs

Date: Mar 9, 2002 12:06 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

#### Command line parameters:

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#### seq\_documentation\_block:

ID AAB01942 standard; Protein; 441 AA.

AC AAB01942;

DT 18-SEP-2000 (first entry)

DE Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).

XX Human; low density lipoprotein associated phospholipase A2;

KW LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;

KW short chain phospholipid; serine dependant phospholipase;

KW inflammation; proinflammatory; anti inflammatory; drug screening;

KW antibody; diagnosis.

OS Homo sapiens.

XX WO200024910-A1.

PN 04-MAY-2000.

PF 27-OCT-1999; 99WO-GH03551.

PR 28-OCT-1998; 98GB-0023647.

PR 28-OCT-1998; 98GB-0023648.

XX (SMK) SMITHKLINE BEECHAM PLC.

PI Boyd H, Tew DG;

XX WPI; 2000-350749/30.

DR N-PSDB; AAA52357.

XX Recombinant low density lipoprotein associated phospholipase A2, used to produce antibodies for diagnostics, is purified using a Blue Sepharose and Q Sepharose column.

Claim 6b: Page 17: 28pp; English.

The present sequence represents human LDL-PLA2. The invention relates to a method for purifying recombinant low density lipoprotein-associated phospholipase A2 (LDL-PLA2). The method comprises applying a cell extract, supernatant or solution containing the recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue Sepharose column, and applying a process which additionally comprises the prior steps of constructing a vector comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a host cell, isolating the tagged protein from the harvest medium or cell lysate, purifying the protein using a metal matrix affinity column (preferably a nickel column), and removing the histidine tag by protease cleavage. LDL-PLA2, also known as plasma PAF acetyl hydroxylase, is a serine-dependent phospholipase which catalyses the hydrolysis of phospholipids with short chain acyl groups at the sn-2 position. Its in vivo role is not known due to its ability to hydrolyse both phospholipids with short chain sn-2 substituents (which often arise from oxidative cleavage of longer chain sn-2 substituents) and PAF. It may be either a pro-inflammatory enzyme or an anti-inflammatory enzyme, depending on the precise in vivo role adopted. LDL-PLA2 can be used in structural and mechanistic studies to elucidate the activity of the enzyme in vivo. The enzyme may be used to screen and identify compounds which modulate its activity, and to raise antibodies for use in diagnostics.

XX Sequence 441 AA;

XX SQ

alignment\_scores:  
 Quality: 2358.00 Length: 441  
 Ratio: 5.347 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
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Align seg 1/1 to: AAB01942 from: 1 to: 441

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98 TGTGTTTATCTTTTACTGGCAATACATAAATCCCTGTTGCCCATATGA 137
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
138 AATCATCAGCATGGCTCAACAAATACAAAGTACTGATGGCTGCTGCAAGC 187
34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50
188 TTTGGCCAACTAAATCCCGGGGAAATCGGCTTATTCGGTTGGTTG 237
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
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101 LysGlnTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
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117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134
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134 rPAsnSerProLeuArgProGlyGlnLysTyrProLeuValValPheSer 150
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151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
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417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
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ID AAR64928 standard; Protein; 442 AA.

AC AAR64928;

XX 18-AUG-1995 (first entry)

XX Human T-cell lymphoma lipoprotein-associated phospholipase-A2.  
 XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;  
 KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.

XX Homo sapiens.

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FT Peptide	368..393
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PN W09500649-A.  
 XX 05-JAN-1995.  
 XX 24-JUN-1994; 94WO-GB01374.  
 XX 25-JUN-1993; 93GB-0013144.  
 PR 11-JAN-1994; 94GB-0000413.  
 XX (SMK) SMITHKLINE BEECHAM PLC.  
 XX Gloger IS, Hickey DMB, Lawrence GMP, Macphree CH;  
 PI Rice SQJ, Southern CD, Tew DG;  
 XX WPI: 1995-052086/07.  
 DR N-PSDB; AAQ81780.  
 XX  
 PT Purified lipoprotein associated phospholipase A2 - used to  
 PT develop prods. for diagnosis and therapy, partic. inhibitors for  
 PT treatment of atherosclerosis  
 XX  
 PS Claim 8; Page 19; 29pp; English.  
 XX  
 CC This sequence encodes an enzyme which may be used in a method of  
 CC screening compounds to identify those compounds which inhibit  
 CC Lp-PLA2 which involves contacting isolated Lp-PLA2 with a test  
 CC compound and measuring the rate of turnover of an enzyme substrate  
 CC as compared with the rate of turnover in the absence of the test  
 CC compound.  
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 Percent Similarity: 100.000 Percent Identity: 100.000

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ID AAR71913 standard; Protein; 441 AA.

AC AAR71913;

DT 05-DEC-1995 (first entry)

XX Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

KW Homo sapiens.

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-0511340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder Cl;

XX MPI; 1995-155262/20.

DR N-PSDB; AAQ87947.

XX New nucleic acid encoding platelet activating factor,

PT acetyl:hydrolase - useful in diagnosis and for treating

PT inflammatory diseases, e.g. pleurisy

XX Claim 5; Page 53-54; 88pp; English.

XX The human acetyl hydrolase gene (AAQ87947) has been isolated and

CC purified. The platelet activating factor acetyl hydrolase (AAR71913)

CC is useful in the treatment of inflammatory diseases, in particular

CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in

CC raising monoclonal antibodies specific for PAF-AH that are useful in

CC the diagnosis of such diseases.

XX Sequence 441 AA;

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Ratio: 5.338

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Length: 441

Gaps: 0

Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAR71913

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188 TTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCCGTTGGTTG 237

51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCys 67

238 TACAGACTTAATGTTTGATCACACTAAATAAGGGCACCTTCCTTCGCTTAT 287

67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84

288 ATTATCCATCCCAAGATAATGATCGCTTGACACACCTTTGGATCCCAAT 337

84 yTyrProSerGlnAspAsnArgLeuAspThrLeuTrpIleProAsn 100

338 AAAGATATATTTTGGGCTTTAGCAAAATTTCTTGAACACACTGCTTAT 387

101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeu 117

388 GGGCAACATTTTGGAGTTACTCTTTGGTTCAATGACAACTCCTGCAAACT 437

117 tGlyAsnIleLeuArgLeuPheGlySerMetThrThrProAlaAsnT 134

438 GGAATTCCTCCTGAGGCTGGTGAATAATATCCACTTGTGTTTCTTCT 487

134 rPasnSerProLeuArgProGlyGluLysTyrProLeuValIlePheSer 150

488 CATGCTCTTGGGGCATTCAGGACACTTTTATTCTGCTATTGGCATTGACT 537

151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167

538 GCATCTCATGGTTTATAGTTGCTGCTGTAGAACACACAGATAGACTG 587

167 uAlaSerHisGlyPheIleValAlaIleValGluHisArgAspArgSer 184

588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637

184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200

638 AAGTCTTGCTCTACCTTAGAACCTGAAACAAGAGGAGGAGACACATAT 687

201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217

688 AGCAATCAGCAGGTACGGGAAAGAGCAAAAGAAATGTTCCCAAGCTCTCA 737

217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeu 234

738 GTCTGATTCTTTGACATTGATCATGGAAGCCAGTGAAGAAATGCAATTAGAT 787

234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250

788 TTAAGTTTGATATGGACAACTCAAGCACTCTATTGATAGGGAATAAT 837

251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267

838 AGCAGTAAATTCGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTA 887

267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeu 284

888 GTGAAGATCAGAGATTCAGATGCTGATTCCTCGGATGATGATGATTTT 937

284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaIlePhePhe 300

938 CCATCTGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTCTTTTAT 987

301 ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheI 317

988 CAACCTCTGAATATTTCCAAATATCTGCTAAATATATCAATAAATAAAT 1037

317 eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLys 334

1038 GCTACTCACCTGATGAAGAAAGAAAGATGATTACATCAGGGGTTCAGTC 1087

334 yTyrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350

1088 CACCAGATTTTGCTGACTTCACTTTTGCACAAATGGAATAATGGACA 1137  
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 1138 CAVGTCFAATTAAGGNGACATAGATTCAAAATCCAGCTATTGATCTTA 1187  
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 434 eSerGlyIleGluLysTyrAsn 441

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seq\_documentation\_block:

ID AAW26498 standard; Protein: 441 AA.

AC AAW26498;

DT 05-JAN-1998 (first entry)

DE Human platelet-activating factor acetylhydrolase.

KW Platelet-activating factor acetylhydrolase; PAF-AH; human;  
 inflammation; asthma; pleurisy; necrotising enterocolitis;  
 adult respiratory distress syndrome; therapy.

OS Homo sapiens.

XX US5656431-A.

XX 12-AUG-1997.

XX 06-OCT-1993; 93US-0133803.

XX 07-JUN-1995; 95US-0483232.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX Wilder CL;

XX WPI; 1997-414580/38.

XX N-PSDB; AAT87048.

XX Detecting lesions in human platelet-activating factor  
 acetylhydrolase gene - by comparison with defined wild-type gene  
 sequence

XX Example 3; Column 47-50; 53pp; English.

XX This polypeptide comprises human plasma platelet-activating factor  
 acetylhydrolase (PAF-AH), a protein that inactivates PAF and  
 inactivates oxidatively fragmented phospholipids such as products of  
 the arachidonic acid cascade that mediate inflammation. Its  
 sequence was deduced from a full-length cDNA clone (see AAT87048)  
 obtained from a macrophage cDNA library. Mouse, dog, cattle,  
 chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have

CC also been identified. Recombinant PAF-AH polypeptides can be  
 produced in prokaryotic or eukaryotic host cells and used to mimic  
 or augment normal processes of resolution of inflammation in vivo.  
 CC Examples describe the in vivo therapeutic effect of recombinant  
 PAF-AH products on acute inflammation, pleurisy, asthma,  
 CC necrotising enterocolitis and adult respiratory distress syndrome  
 CC in animal models.

XX Sequence 441 AA;

alignment\_scores:

Quality: 2354.00 Length: 441

Ratio: 5.348 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAW26498 ..

Align seg 1/1 to: AAW26498 from: 1 to: 441

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 |||||  
 1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17  
 |||||  
 88 TCTGTTTATCTCTTTGACTGGCAATACATAAATCCCTGTTGCCCATATGA 137  
 |||||  
 17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
 |||||  
 138 AATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCGCAACC 187  
 |||||  
 34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaIleSer 50  
 |||||  
 188 TTTGGCCAAACTTAAATCCCGGGGAAATGGCCCTTATTCCGTTGGTTG 237  
 |||||  
 51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67  
 |||||  
 238 TACACACTTAATGTTTGTATCATCAGCTAATAAGGCACCTTCTTGGCTTTAT 287  
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 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
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 84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
 |||||  
 338 AAAGATATATTTTGGGCTCTPAGCAAAATTTCTTGGACACACACTGCTTAT 387  
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 101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117  
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 438 GGAATTCCTCTCTGAGGCTGCTGGAANAATATCCACTTGTGTTTCTTCT 487  
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 134 rPasnSerProLeuArgProGlyGluLysTyrProLeuValValPheSer 150  
 |||||  
 488 CATGTCTCTTGGGCAATTCAGGACACTTTTATTCTGCTATTGGCATTGACCT 537  
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 151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167  
 |||||  
 538 GGCATCTCATGGCTTATAGTTGCTGCTAGAACACACAGAGATAGATCTG 587  
 |||||  
 167 uAlaSerHisGlyPheIleValAlaValAlaGluHisArgAspArgSera 184  
 |||||  
 588 CATCTCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637  
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 184 IaSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200  
 |||||  
 638 AACTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGAGAGGAGACACATAT 687  
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 201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217  
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738 GCTGATCTTTGACATTTGATCATGCAAGCCAGTGAAGAATGCATTAGAT 787
|||||
234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
|||||
788 TTAAGTTTGATATGACACACTGAAGACTCTATTGATAGGAAAAAT 837
|||||
251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysII 267
|||||
838 AGCAGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTA 887
|||||
267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284
|||||
888 GTGAAGATCAGAGATTCAGATGCTGGTATGCGCTGGATCGATGATGTT 937
|||||
284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
|||||
938 CCACGTGGGTGATGAAGTATATCCAGAAATTCCTCAGCCCTCTTTTAT 987
|||||
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988 CAACCTCTCAATATTTCCAAATCTCTGCTTAATCATATAAATGAAAAAT 1037
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317 eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
|||||
1038 CCTACTACCTGATTAACAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
|||||
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|||||
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367 smetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384
|||||
1188 GCAACAAAGCTTCATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAA 1237
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384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
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401 AspPheAspGlnTyrPaspCysLeuIleGluGlyAspAspGluAsnLeuII 417
|||||
1288 TCCAGGACCAACATTAAACACCAATCAACATCATGTTTACAGAACT 1337
|||||
417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
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1338 CTTCCAGGAATAGAGAAATACAAT 1360
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434 erSerGlyIleGluLysTyrAsn 441
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seq\_name: /SDS2/gcgdata/geneseq/geneseq/AA1997.DAT:AAW23796

seq\_documentation\_block:

ID AAW23796 standard; Protein; 441 AA.

XX

AC AAW23796;

XX

DT 04-NOV-1997 (first entry)

XX

DE Human plasma platelet activating factor acetylhydrolase.

XX Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;

KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;

KW central nervous system shock; arthritis; Crohn's disease;

KW systemic lupus erythematosus; adult respiratory distress syndrome.

XX Homo sapiens.

OS

XX US5641669-A.  
PN XX  
PD 24-JUN-1997.  
XX  
PF 06-OCT-1993; 93US-0133803.  
XX  
PR 06-OCT-1994; 94US-0318905.  
PR 06-OCT-1993; 93US-0133803.  
XX  
PA (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
PI Wilder CL;  
PI  
XX WPI; 1997-340947/31.  
DR N-PSDB; AAT80564.  
XX

XX New human plasma platelet activating factor acetylhydrolase -  
PT useful as anti-inflammatory for treatment of asthma, anaphylaxis,  
PT shock, etc  
XX  
PS Claim 1; Column 35-38; 43pp; English.

XX The present sequence represents the purified and isolated human plasma  
CC platelet activating factor acetylhydrolase (PAF-AH). This novel  
CC polypeptide inactivates PAF and oxidatively fragmented phospholipids  
CC such as pro-inflammatory arachidonic acid metabolites, and so can be  
CC used to treat inflammation by augmenting endogenous activity. Typical  
CC applications are in asthma, anaphylaxis, shock, reperfusion injury,  
CC central nervous system shock, arthritis, Crohn's disease, systemic  
CC lupus erythematosus, adult respiratory distress syndrome. The  
CC polypeptide can also be used to raise specific antibodies (Ab) which  
CC are useful as immunoassay reagents and for generating anti-idiotypic  
CC antibodies. The nucleic acid encoding the protein can be used to screen  
CC for related genes; in hybridisation assays to assess the protein-  
CC producing cells; to generate knockout mice; to detect genetic mutations  
CC and (antisense sequences) to inhibit the protein expression. Unlike PAF  
CC receptor antagonists, the protein is a natural component of plasma.  
XX  
SQ Sequence 441 AA;

alignment\_scores:

Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAW23796

Align seg 1/1 to: AAW23796 from: 1 to: 441

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|||||  
1 MetValProProLysLeuHisValLeuPheCysLeuGlyCysLeuAl 17  
88 TGTGCTTTATCTTTTGTGACTGGCAATACATAAATCCCTGTTGCCCATATGA 137  
|||||  
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
|||||  
138 AATCATCAGCATGGTGCACAAAATACAACTACATGCTGCTGCTGAAGC 187  
|||||  
34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaIaser 50  
|||||  
188 TTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCTGCTGGTTCG 237  
|||||  
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67  
|||||  
238 TACAGACTTAAATGTTTGCATCACACTAATAAGGCGACCTTCTTCGCTTAT 287  
|||||  
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84



288 ATTATCCATCCCAAGATATATGATCGCTTGGACACCTTTGGATCCCAAT 337  
 |||||  
 84 yTyProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
 |||||  
 338 AAAGAATATTTTGGGGCTTACGAAATTTCTTGGACACACTGGCTTAT 387  
 |||||  
 101 LysGluTyPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeu 117  
 |||||  
 388 GGCAACATTTTGGAGTTACTCTTTGGTTCATGACAACTCCTCAAACT 437  
 |||||  
 117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134  
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 438 GGAATCCCTCTGAGGCTGCTGAGAAATATCCACTTGTGTTTCT 487  
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 134 rPAsnSerProLeuArgProGlyGluLysTyProLeuValValPheSer 150  
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 488 CATGCTTTGGGCACTTACAGACACTTATTCTGCTATTGGCATTGACCT 537  
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 151 HisGlyLeuGlyAlaPheArgThrLeuTySerAlaIleGlyIleAspLe 167  
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 1288 TCAGGAGCACCACATTAAACACACCAATCAACACATCATGTTACAGAACT 1337  
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seq\_name: /SIDS2/qcydata/geneseq/geneseq/AA1997.DAT:AAW09808

seq\_documentation\_block:

ID AAW09808 standard; Protein; 441 AA.

XX AAW09808;

DT 12-JUN-1997 (first entry)

XX Platelet-activating factor acetylhydrolase.

XX Human platelet-activating factor acetylhydrolase; PAF-AH; detection;  
 KW mutation; V279F; substitution; restriction fragment length polymorphism;  
 KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;  
 KW asthmatic children; treat; inflammatory condition.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..41  
 FT /label= signal\_peptide  
 FT /note= "possibly contains additional peptide that is  
 FT cleaved to yield the mature functional enzyme"

FT Protein 42..441

FT /label= mature\_enzyme

FT Active-site 271..275

FT /note= "contains active site serine; conforms to  
 FT consensus motif for mammalian and microbial  
 FT lipases and serine proteases"

XX US5605801-A.

XX 25-FEB-1997.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

PR 06-OCT-1993; 93US-0133803.

PR 07-JUN-1995; 95US-0478465.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

PI Wilder CL;

XX WPI; 1997-153573/14.

DR N-PSDB; AAT63701.

XX Detection of platelet-activating factor acetylhydrolase gene  
 mutation - by restriction length polymorphism analysis

PT Example 3; Column 33-38; 43pp; English.

PS This sequence is that of human platelet-activating factor acetyl-  
 CC hydrolase (PAF-AH).  
 CC The claimed method of the invention detects a mutation (which results  
 CC in a V279F substitution) in the PAF-AH gene, and comprises performing a  
 CC restriction fragment length polymorphism analysis and differentiating

CC between wild-type and mutant alleles on the basis of the number of  
 CC restriction sites. The method is useful for diagnosis of inherited PAF-AH  
 CC deficiency, which has been correlated with severe respiratory symptoms in  
 CC asthmatic children. Recombinant PAF-AH can be used to treat inflammatory  
 CC conditions.

XX  
 SQ Sequence 441 AA:

alignment\_scores:  
 Quality: 2354.00 Length: 441  
 Ratio: 5.338 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAW09808

Align seg 1/1 to: AAW09808 from: 1 to: 441

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|||||
1 MetValProProlysLeuHisValLeuPheCysLeuCysGlyLeuAl 17
88 TGTGGTTTATCCCTTTGACTGGCAATACATAAATCCTGTTGCCATATGA 137
|||||
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
138 AATCATCAGCATGGTCAACAAATACAAAGTACTGATGGCTGCTGCAAGC 187
|||||
34 YsserSerAlatrPvalAsnLysIleGlnValLeuMetAlaLaLaSer 50
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338 AAAGAATATTTTGGGCTCTAGCAAAATTTCTGGAACACACTGGCTTAT 387
|||||
101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
388 GGGCACATTTTGGGTTACTCTTTGGTTCAATGACAACTCCTGCAAACT 437
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117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134
438 GGAATTCCTCTCGAGGCTGGTGAATAATATCCACTGTTGTTTCTTCT 487
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134 rPasnSerProLeuArgProGlyGluLysTyrProLeuValValPheSer 150
488 CATGGTCTTGGGCATTCAGGACACTTTATTTCTGCTATTGGCAATTGACCT 537
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151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
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|||||
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSera 184
588 CATCTGCCAATCTACTATTTCAGGACCACCAATCTGCTGCAGAAATAGGGAC 637
|||||
184 LeSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200
638 AAGCTCTGGCTCTACCTTAGACCCCTGAAACAGAGGAGGAGACACATAT 687
|||||
201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisIle 217
688 ACGAATAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCA 737
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234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
788 TTAAGTTTGTATATGGAACAACTGAAGGACTCTATTGATAGGGGAAAAAT 837
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251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267
838 AGCAGTAATTCGACATCTTTTGTGCTGGAGCAACGGTTATTTCAGACTCTTA 887
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267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284
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284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
938 CCATCTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTAT 987
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988 CAATCTGAATATTTCCAATATCCTGCTAATATCATAAATGAAAAAT 1037
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317 eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
1038 GCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGGTTCAGTC 1087
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334 YsTyrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350
1088 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCACCTGGCAAAATATTTGGACA 1137
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384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
1238 GATTTTTCATCAGTGGGACTGCTTTCATTGAGGAGATGATGAGAATCTTAT 1287
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401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuI 417
1288 TCCAGGACCAACATTAACACAAACCAATCAACATCATCTGTTACAGAACT 1337
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417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
1338 CTTTCAGGAATAGAGAAATACAAT 1360
434 erSerGlyIleGluLysTyrAsn 441

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seq\_name: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT:AAW38361

seq\_documentation\_block:

ID AAW38361 standard; Protein; 441 AA.

XX AAW38361;

XX

DT 31-MAR-1998 (first entry)

XX

DE Human plasma platelet activating factor acetylhydrolase.

XX Human: plasma platelet activating factor acetylhydrolase;

KW monoclonal antibody; immunoassay; diagnosis; asthma;

KW detection.

XX

OS Homo sapiens.

XX

PN US5698403-A.

XX

PD 16-DEC-1997.  
 PF 07-JUN-1995; 95US-0483140.  
 XX 06-OCT-1994; 94US-0318905.  
 PR 06-OCT-1993; 93US-0133803.  
 PR 07-JUN-1995; 95US-0483140.  
 XX (ICOS-) ICOS CORP.  
 PA Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
 XX Wilder CL;  
 PI WPI: 1998-051484/05.  
 XX N-PSDB; AAT96127.  
 DR Immunossay for platelet activating factor acetylhydrolase, PAP-AH  
 XX - useful to diagnose disorders associated with abnormal PAP-AH level  
 PT Claim 1; Columns 35-38; 47pp; English.  
 PS The present sequence was used in the development of a method for  
 CC detecting human, mouse, canine, rat and monkey plasma platelet  
 CC activating factor acetylhydrolases (PAP-AH). The method comprises  
 CC contacting serum with PAP-AH specific monoclonal antibody (Mab) to  
 CC form a PAP-AH/MAB complex, and detecting the complex. The method  
 CC can be used to diagnose disorders associated with abnormal PAP-AH  
 CC levels, and to monitor therapy of such disorders. Plasma PAP-AH  
 CC deficiency has been correlated with severe respiratory symptoms in  
 CC asthmatic children who appear to have inherited the deficiency in  
 CC an autosomal recessive manner.  
 XX Sequence 441 AA;

alignment\_scores:  
 Quality: 2354.00 Length: 441  
 Ratio: 5.338 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.773  
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 17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
 138 AATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGCTGCAAGC 187  
 34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
 188 TTTGCGCAAACTAAATCCCGCGGAAATGGGCTTATTCGCTTGTTGTTG 237  
 51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67  
 238 TACAGACTTAATGTTTATGATCAGACTAATAAGGCGACCTTCTGCGTTTAT 287  
 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
 288 ATTATCCATCCCAAGATAATGATGCTGACACCTTGCACACCTTTGGATCCCAAT 337  
 84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
 338 AAAGAATATTTTGGGTCTTAGCAAAATTTCTTGGAACACACATGGCTTAT 387  
 101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117

388 GGCAACATTTTGGAGTTTACTCTTTGCTTCAATGACAACTCTCTGCAACT 437  
 117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134  
 438 GGAATTCCTCTCTGAGCGCTGGTGAAATAATATCCACTGTTGTTTCTTCT 487  
 134 rPAsnSerProLeuArgProGlyGlyLysTyrProLeuValValPheSer 150  
 488 CATGCTCTTGGGCGATTCAGGACACTTTATTCTGCTATTGGCATTTGACCT 537  
 151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167  
 538 GGCATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTG 587  
 167 uAlaSerHisGlyPheIleValAlaValGluHisArgAspArgSerA 184  
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 184 lAsrAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200  
 638 AAGCTCTGCTCTTACCTTAGAACCTGAAACAGAGAGAGAGACATAT 687  
 201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217  
 688 AGCAATGAGCAGGTACGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCA 737  
 217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeu 234  
 738 GTCTGATCTTTCACATTCATGATGGAAGCCAGTGAAGATGCATTTAGAT 787  
 234 eTLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250  
 788 TTAAGTTTGTGATATGGAACAACACTGAAGACTCTATTGATAGGAAAAAT 837  
 251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267  
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 301 ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheI 317  
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seq\_documentation\_block:

ID AAW96334 standard; Protein; 441 AA.

AC AAW96334;

28-JUN-1999 (first entry)

Human plasma platelet-activating factor acetylhydrolase (PAF-AH).  
 Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;  
 platelet activating factor; inflammation; treatment; hydrolysis;  
 augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;  
 acute respiratory distress syndrome; pancreatitis;  
 neurological disease; HIV; human immunodeficiency virus.

OS Homo sapiens.

XX WO9909147-A1.

PN 25-FEB-1999.

PD 13-AUG-1997; 97WO-US14212.

XX 13-AUG-1997; 97WO-US14212.

PR (ICOS-) ICOS CORP.

PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
 PI Wilder CL;

XX WPI; 1999-181028/15.

DR N-PSDB; AAX08463.

XX New truncated human platelet-activating factor acetylhydrolase and  
 PT its encoding polynucleotides - useful for regulating inflammatory  
 PT events

PS Claim 1; Page 97-98; 136pp; English.

XX Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be  
 CC used to inactivate the pathological effects of PAF.  
 CC Pathological conditions which can be treated include pleurisy,  
 CC asthma, rhinitis, necrotizing enterocolitis, acute respiratory  
 CC distress syndrome, acute pancreatitis or neurological disease  
 CC associated with HIV infection. Identification and isolation of  
 CC polynucleotide sequences encoding human plasma PAF-AH allows the  
 CC recombinant production of PAF-AH. This makes possible the use of  
 CC exogenous PAF-AH to mimic or augment normal processes of resolution  
 CC of inflammation in vivo. PAF inactivation occurs by hydrolysis of  
 CC the PAF sn-2 acetyl group by PAF-AH. PAF-AH also metabolises  
 CC oxidatively fragmented phospholipids such as products of the  
 CC arachidonic acid cascade which mediate inflammation. Administration  
 CC of PAF-AH is advantageous to administering PAF receptor antagonists  
 CC since PAF-AH is a product normally found in plasma. Because PAF  
 CC receptor antagonists are structurally related to PAF they  
 CC competitively inhibit native PAF-AH activity. Treatment with  
 CC recombinant PAF-AH would augment endogenous PAF-AH activity and  
 CC compensate for any inactivated endogenous enzyme.

XX Sequence 441 AA;

alignment\_scores:  
 Quality: 2354.00

Length: 441

Percent Similarity: 100.000 Gaps: 0  
 Ratio: 5.338 Percent Identity: 99.773  
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 17 aValValTyrProPheAspTgPInTyrIleasnProValAlaHisMetL 34  
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1238 GATTTTCATCAGTGGGACTGCTGTGATTGAGGAGATGATGAGAACTTTAT 1287  
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1288 TCCAGGACCAACATTACACACACCAATCAACACATCATGTTTACAGAACT 1337  
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1338 CTTTCAGCAATAGAGAAATCAAT 1360  
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434 erSerGlyIleGluLysTyrAsn 441

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seq\_documentation\_block:

ID AAW73359 standard; Protein; 441 AA.

AC AAW73359;

XX

XX 12-FEB-1999 (first entry)

DT Human PAF-AH protein sequence.

DE Platelet-activating factor acetylhydrolase; PAF-AH; human; antibody.

XX Homo sapiens.

XX US5847088-A.

XX 08-DEC-1998.

XX 07-JUN-1995; 95US-0485938.

XX 07-JUN-1995; 95US-0485938.

PR 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX Wilder CL;

PI

XX

DR WPI; 1999-059148/05.  
XX N-PSDB; AAV08534.  
PT Antibodies specific for platelet-activating factor acetylhydrolase  
XX proteins - useful for detecting or purifying the proteins  
XX Claim 1; Column 45-48; 59pp; English.  
XX This sequence represents the human platelet-activating factor  
XX acetylhydrolase (PAF-AH). This protein is specifically bound by  
XX the antibody of the invention. The monoclonal antibody of the invention  
XX is useful for detecting or purifying PAF-AH proteins.  
XX Sequence 441 AA:

alignment\_scores:  
Quality: 2354.00 Length: 441  
Ratio: 5.338 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 99.773  
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US-09-922-067-9 x AAW73359 ..

Align seg 1/1 to: AAW73359 from: 1 to: 441

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88 TGTGTTTATCTCTTTGACTGGCAATACATAAATCCCTGTTGCCCATATGA 137  
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17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
138 ANTCAATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGCTGCAAGC 187  
|||||  
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188 TTTGGCCAACTAAATCCCCGGGAAATGGGCTTATTCGGTTGGTTG 237  
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seq\_documentation\_block:

ID AAB07774 standard; Protein: 441 AA.

AC AAB07774;

XX 14-NOV-2000 (first entry)

XX Plasma platelet-activating factor acetylhydrolase.

XX Platelet-activating factor acetylhydrolase; platelet-activating factor;

KW reperfusion injury; acute inflammation; pleurisy; asthma;  
 KW necrotising enterocolitis; adult respiratory distress syndrome.  
 XX Homo sapiens.  
 OS US6099836-A.  
 PN 08-AUG-2000.  
 PD 19-JUN-1998; 98US-0100546.  
 PF 07-JUN-1995; 95US-0480658.  
 PR 22-JAN-1998; 98US-0010715.  
 PR 06-OCT-1993; 93US-0133803.  
 PR 06-OCT-1994; 94US-0318905.  
 XX (ICOS-) ICOS CORP.  
 PA Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;  
 XX Cousins LS;  
 PI WPI: 2000-531654/48.  
 PI N-PSDB; AAA59579.  
 XX DR  
 DR  
 XX  
 PS Treating mammal susceptible to or suffering from platelet-activating  
 PT factor mediated condition associated with reperfusion injury such as  
 PR acute inflammation, pleurisy, asthma, necrotising enterocolitis -  
 XX Example 3; Column 49-52; 55pp; English.  
 XX The specification describes a pharmaceutical composition comprising  
 CC platelet-activating factor acetylhydrolase. The composition is  
 CC administered for treating a mammal susceptible to or suffering from  
 CC a platelet-activating factor-mediated condition associated with  
 CC reperfusion injury. Diseases and conditions which may be treated  
 CC include acute inflammation, pleurisy, asthma, necrotising enterocolitis  
 CC and adult respiratory distress syndrome. The present sequence represents  
 CC human plasma platelet-activating factor acetylhydrolase.  
 XX  
 SQ Sequence 441 AA;

alignment\_scores:  
 Quality: 2354.00 Length: 441  
 Ratio: 5.338 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAB07774

Align seg 1/1 to: AAB07774 from: 1 to: 441

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 |||  
 1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17  
 |||  
 88 TGTGGTTTATCTTTTGTGCTGGCAATACATAAAATCCTGTTGCCCATATGA 137  
 |||  
 17 aValValTyrlProPheAspTrpGlnTyrlIleAsnProValAlaHisMetL 34  
 |||  
 138 AATCATCAGCATGGCTCAACAAATACAAATACATGATGCTGTGCTGCAAGC 187  
 |||  
 34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
 |||  
 188 TTTGGCCAAACTAAATCCCGGGGAAATGGCGCTTATTCCCTGTGGTTG 237  
 |||  
 51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrlSerValGlyCy 67  
 |||  
 238 TACAGACTTAATGTTTGTATCAGACTTAATAGGGCACCCTTCTTGGGTTTAT 287  
 |||  
 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84  
 |||  
 288 ATTATCCATCCCAAGATAATGATCGCTTGACACACCCCTTTTGGATCCCAAAAT 337

|||||  
84 yTrpProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
|||||  
338 AAGAATATATTTTGGGGCTTACGAAATTTCTTGGAAACACACTGGCTTAT 387  
|||||  
101 LysGluTyrrPheTrpGlyLeuSerTyrsPheLeuGlyThrHisTrpLeuMe 117  
|||||  
388 GCGCAACATTTTTCAGCTTACTCTTCTTGGTTTCAATGACAACTCTCGAAACT 437  
|||||  
117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134  
|||||  
438 GGAATTTCCCTCTGAGGCTGTGGAATATCCACTTGTGTTTTTCT 487  
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134 rPAsnSerProLeuArgProGlyGlyLeuTyrrProLeuValValPheSer 150  
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488 CATGGCTCTTGGGCATTACAGGACACCTTATCTGCTATTGCGATTGACCT 537  
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151 HisGlyLeuGlyAlaPheArgThrLeuTyrrSerAlaIleGlyIleAsp 167  
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538 GGCATCTCATGGGTTTATAGTTCCTGCTCTGACACACAGATAGATCTG 587  
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167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSer 184  
|||||  
588 CATCTGCAACTTACTATTTCAGAGACCAATCTGCTGCAGAAATAGGGAC 637  
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184 laSerAlaThrTyrrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200  
|||||  
638 AGTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGGAGGAGACACATAT 687  
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201 LysSerTrpLeuTyrrLeuArgThrLeuLysGlnGluGluThrHisI 217  
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688 ACGAAATGACAGCTACGGCAAGACCAAAAGAAATGTTCCCAAGCTCTCA 737  
|||||  
217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeu 234  
|||||  
738 GTCTGATCTTGATGATGATGATGGAAGCCAGTGAAGATGCTAGAT 787  
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234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250  
|||||  
788 TTAAGCTTTCATATGAAACAACTGAAGGACTCTATTATGATAGGAAAAAT 837  
|||||  
251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267  
|||||  
838 AGCAGTAATTTGGACATCTTTTGGTGGAGCAGCAGCGTTATTACAGCTCTTA 887  
|||||  
267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeu 284  
|||||  
888 GTGAAGATCAGAGATTACAGATGGGTATTGCTGCTGATGATGATGTTT 937  
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284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300  
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938 CCACCTGGGTGATGAATATATCCGAATTCCTACGCCCTCTTTTTTAT 987  
|||||  
301 ProLeuGlyAspGluValTyrrSerArgIleProGlnProLeuPhePheI 317  
|||||  
988 CAATCTCGAATATTTCCAAATATCTCTCTAATATCATAAAAAATGAAAAAT 1037  
|||||  
317 eAsnSerGluTyrrPheGlnTyrrProAlaAsnIleLysMetLysLysC 334  
|||||  
1038 GCTACTCACCTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 1087  
|||||  
334 yTrpSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350  
|||||  
1088 CACCAGAAATTTCTCAGCTTCACTTTTGAACCTGGCAAAATATTCGACA 1137  
|||||  
351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleGlyHis 367  
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1138 CATGCTCAAAATTAAGGGAGACATAGATTCAATGCAGCTATTTGATCTTA 1187  
|||||  
367 sMetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeu 384  
|||||  
1188 GCACCAAGCTTCATTAGCATCTTCTTCAAAAGCATTTAGGACTTCATAA 1237  
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384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400  
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1238 CATTTTCATCAGTGGGACTGCTTCATTGAAGGAGATGATGAGAACTTAT 1287  
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401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuI 417  
|||||  
1288 TCCAGGACCAACATTAACACACAAATCAACACATCATCTTACAGAACT 1337  
|||||  
417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsn 434  
|||||  
1338 CTTTCAGCAATAGAGAAATACAAT 1360  
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434 erSerGlyIleGluLysTyrrAsn 441

seq\_name: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:AAy88301

seq\_documentation\_block:

ID: AAy88301 standard; Protein; 441 AA.

XX AC AAy88301;

XX XX 14-JUL-2000 (first entry)

XX Human platelet-activating factor acetyl hydrolase amino acid sequence.  
XX Platelet-activating factor acetyl hydrolase; PAF-AH: PAF: phospholipid;  
KW inflammatory response; pre-term labour; pharmaceutical composition;  
KW regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease;  
KW pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.

OS Homo sapiens.

XX XX US6045794-A.

XX PN XX 04-APR-2000.

XX PD XX 09-JUN-1999; 99US-0328474.

XX PF XX 12-AUG-1997; 97US-0910041.

XX PR XX 06-OCT-1993; 93US-0133803.

XX PR XX 06-OCT-1994; 94US-0318905.

XX PR XX 07-JUN-1995; 95US-0483232.

XX PA (ICOS-) ICOS CORP.

XX XX Cousens LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;

XX PI Eberhardt CD;

XX XX WPI: 2000-282671/24.

XX DR N-PSDB; AAL0861.

XX PT Treatment of mammals suffering from pre-term labour comprises

XX PT administering a pharmaceutical composition comprising

XX PT platelet-activating factor acetyl hydrolase enzyme -

XX PS Claim 1; Column 67-70; 67pp; English.

XX CC This sequence represents the human platelet-activating factor acetyl  
XX CC hydrolase (PAF-AH) amino acid sequence. PAF is a phospholipid and is  
XX CC implicated in pathological inflammatory responses (e.g. asthma,  
XX CC anaphylaxis, septic shock and arthritis). PAF-AH is released by  
XX CC hepatocytes, and macrophages and inactivates PAF. PAF-AH also inactivates  
XX CC oxidatively fragmented phospholipids that mediate inflammation. This  
XX CC sequence is specifically claimed for use in a method to treat a mammal  
XX CC suffering from pre-term labour. PAF-AH is included in a pharmaceutical  
XX CC composition which can be administered to a mammal suffering from pre-term  
XX CC labour. The invention relates to purified and isolated polynucleotide  
XX CC sequences encoding human PAF-AH and materials and methods for the  
XX CC recombinant production of PAF-AH products which are expected to be useful  
XX CC in regulating inflammatory events. The administration of PAF-AH to  
XX CC animals may be used for ameliorating pathological inflammatory conditions  
XX CC such as asthma, anaphylaxis, shock, arthritis, Crohn's disease,  
XX CC pancreatitis, allergic inflammation, and human immunodeficiency virus

234	erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp	250
788	TTAAAGCTTTGATATGGAAACAACATGAAGAGCTCTATTGATAGGGAAAAAAT	837
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838	AGCAGTAANTTGGACATCTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTA	887
267	eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS	284
888	GTGAAGATCAGAGATTTCAGATGTGGTATTGCCCTGGATGCATGCATCTTT	937
284	erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe	300
938	CCACTGGGTGATGAAGATATATCCAGAATTCCTCAGCCCTCTTTTAT	987
301	ProLeuGlyAspGluValTrpSerArgIleProGlnProLeuPhePheIle	317
988	CAACTCTGAATATTTCCATATCTCTCTAATATCATATAAAATGAAAAAT	1037
317	eAsnSerGluTyrrPheGlnTyrrProAlaAsnIleIleLysMetLysLysC	334
1038	GCTACTCACCTGATAAGAAAGAAAGATGATTCAATCAGGGGTTTCAGTC	1087
334	ysTyrrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal	350
1088	CACCAGAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACA	1137
351	HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHis	367
1138	CATGCTCAAAATTAACGGGAGACATAGATTCAAAATGCAGCTATTGACTCTTA	1187
367	MetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS	384
1188	GCAACAAAGCTTCATTAGCATCTTTACAAAAGCATTTAGGACTTCATAAA	1237
384	erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys	400
1238	GATTTTGATTCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAAATCTTAT	1287
401	AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuIle	417
1288	TCAGGGACCAACATTAAACACACCNAATCAACATCATGTTACAGAACT	1337
417	eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS	434
1338	CTTCAGGAATAGAGAAATCAAT	1360
434	erSerGlyIleGluLysTyrrAsn	441
seq_name: /SIDS2/ycgdata/geneseq/geneseq/A2000.DAT:AA50735		
seq_documentation_block:		
ID	AA50735 standard; Protein; 441 AA.	
XX		
AC	AA50735;	
DT	08-FEB-2000 (first entry)	
XX		
DE	Human PAF-AH protein.	
XX		
KW	platelet activating factor acetylhydrolase; PAF-AH; human;	
KW	antiinflammatory; antiasthmatic; antiallergic; antiarthritic;	
KW	anaphylactic; inflammatory disorder; anaphylaxis; ulcerative	
KW	antigen-induced arthritis; ischemia; septicemia; allergy.	
OS	Homo sapiens.	
XX		
PN	U55977308-A.	
XX		
PD	02-NOV-1999.	
XX		
PF	12-AUG-1997; 97US-0910041.	



XX 06-OCT-1993; 93US-0133803.  
 PR 06-OCT-1994; 94US-0318905.  
 PR 07-JUN-1995; 95US-0483232.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;  
 PI Eberhardt CD;  
 XX  
 DR WPI; 2000-021956/02.  
 DR N-PSDB; AAZ24240.  
 XX  
 PT Truncated and substituted versions of human platelet activating factor  
 PT acetylhydrolase, for treating or preventing inflammatory diseases such  
 PT as asthma -  
 XX  
 PS Example 3; Column 63-66; 65pp; English.  
 XX  
 CC This invention describes novel truncated and variant forms (I) of human  
 CC PAF-AH (platelet activating factor acetylhydrolase) which have  
 CC antiinflammatory, antiasthmatic, antiallergic, antiarthritic and  
 CC antiischemic activity. (I) are used to treat a wide variety of  
 CC inflammatory disorders, e.g. asthma, anaphylaxis, antigen-induced  
 CC arthritis, ulcerative colitis, ischemia, septicemia, allergy, etc.  
 CC Recombinant (I), produced in prokaryotic cells, are less heterogeneous  
 CC at the termini than the full-length protein. Some of the truncated  
 CC versions also have greater activity than the wild-type enzyme. This  
 CC sequence represents the human PAF-AH protein which is described in the  
 CC method of the invention.  
 XX  
 SQ Sequence 441 AA;

alignment\_scores:  
 Quality: 2354.00 Length: 441  
 Ratio: 5.338 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 99.773  
 alignment\_block:  
 US-09-922-067-9 x AAY50735 ..  
 Align seg 1/1 to: AAY50735 from: 1 to: 441  
 38 ATGTTGCCACCCAAATGCGTGTTCCTGCTCTGCGGCTGCTGCG 87  
 1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17  
 88 TGTGTTTATCCTTTGACCTGCGCAATACATAAATCCTGTGCGCCATATGA 137  
 17 aValValProPheAspPrpGlnThrIleAsnProValAlaHisMetL 34  
 138 AATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGCTGCAAGC 187  
 34 ysSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
 188 TTTGCCCAACTAAATCCCGGGGAATGGCCCTATTCCGTTGGTTG 237  
 51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTy:SerValGlyCy 67  
 238 TACAGCTTAATGTTGATCACAATAATAAGGCGACCTCTCTGCGTTTAT 287  
 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
 288 ATTATCATCCCAAGATAATGATCGCTTGACACCCCTTTGGATCCCAAT 337  
 84 yTrpProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
 338 AAAGAATATTTTGGGTCTTACAAATTTCTTGGACACACTGGCTTAT 387  
 101 LysGluTyPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117  
 388 GGGCAACACTTTGAGTTACTCTTGTGTTCAATGACAACTCTCTGCAACT 437

117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134  
 438 GGAATTCCTCTCTGAGCCCTGGTGAAATATATCCACTTGTGTTTCTTCT 487  
 134 rpAsnSerProLeuArgProGlyGluLysTyPProLeuValValPheSer 150  
 488 CATGCTCTTGGGCATTCAGGACACATTTATTTCTGCTATTGGCATTGACCT 537  
 151 HisGlyLeuGlyAlaPheArgThrLeuTy:SerAlaIleGlyIleAspLe 167  
 538 GGCATCTCATCGGGTTTATAGTTGCTGCTGTAGACACAGAGATAGATCTG 587  
 167 uAlaSerHisGlyPheIleValAlaValGluHisArgAspArgSerA 184  
 588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637  
 184 laSerAlaThrTyTyPheLysAspGlnSerAlaAlaGluIleGlyAsp 200  
 638 AAGCTTTCGCTCTACCTTAGAACCTGAAACAGAGAGAGAGACACATAT 687  
 201 LysSerTrpLeuTyPLeuArgThrLeuLysGlnGluGluThrHisI 217  
 688 ACCAAATCAGCAGGTACGCCAAGAGCAAAAGATGTTCCCAAGCTCTCA 737  
 217 eaArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234  
 738 GTCTGATTTCTTGACATGATCATGGAAGCCAGTGAAGATGATGATAGAT 787  
 234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250  
 788 TTAAGTTTGATATGGAACAACACTGAAGACTCTATTGATAGGCAAAAT 837  
 251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267  
 838 ACCAGTAATTTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTA 887  
 267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284  
 888 GTGAAGATCAGAGATTCAGATCTGATTTGCTGCTGCTGATGATGATGTTT 937  
 284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300  
 938 CCACCTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTAT 987  
 301 ProLeuGlyAspGluValTy:SerArgIleProGlnProLeuPhePheI 317  
 988 CAACCTCTGAATATTTCCAAATATCTCTGCTTAATATCATAAATGAAAT 1037  
 317 eaSnSerGluTyPheGlnTyPProAlaAsnIleIleLysMetLysLysC 334  
 1038 GCTACTCACCTCATAAAGAAAGAGATGATTACAAATCAGGGTTCAGTC 1087  
 334 yTyTySerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350  
 1088 CACCAGAAATTTTCTGACTTCACCTTTTGCACACTGGCAAAATTAATGGACA 1137  
 351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHi 367  
 1138 CATGCTCAAAATTAAGGGAGACATAGATTCAATGTCAGCTATTGATCTTA 1187  
 367 sMetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384  
 1188 GCAACAAAGCTTCATTAGCATTTCTTACAAAGCATTTAGAGCTTCATATA 1237  
 384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400  
 1238 GATTTTGTATCAGTGGGACTGCTTGTGATGAAGAGATGATGAGATCTTAT 1287  
 401 AspPheAspGlnTrpAspCysIleGluGlyAspAspGluAsnLeuI 417  
 1288 TCCAGGACCAACANTTAACACAACCAATCAACACATCATGTTACAGAACT 1337

417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434

1338 CTTGAGGAAATACAGAAATACAAAT 1360

434 eISerGlyIleGluLysTrpAsn 441

seq\_name: /SIDS2/gcdata/geneseq/geneseq/AA2001.DAT:AAE00761

seq\_documentation\_block:

ID AAE00761 standard; Protein: 441 AA.

AC AAE00761;

DT 02-JUL-2001 (first entry)

XX Human plasma platelet-activating factor acetylhydrolase (PAF-AH).

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
XX antiinflammatory; septicemia; inflammation; haemostasis; parturition;  
KW asthma; anaphylaxis; septic shock; antibacterial.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..41

FT /note= "Hydrophobic segment containing 1-17 amino acids  
FT of signal sequence plus an additional peptide that is  
FT cleaved to yield the mature functional enzyme"

FT Protein 42..441

FT /label= Mature\_human\_PAF-AH\_peptide

FT Domain 271..275

FT /label= Consensus\_motif

XX US6203790-B1.

PN 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

PR 22-JAN-1998; 98US-0010715.

PR 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

PA Cousins LS, Eberhardt CD, Gray P, Trong HL, "Joelker LW;  
PI Wilder CL;

PI WPI; 2001-280610/29.

DR N-PSDB; AAD04143.

XX Treating a mammal susceptible to or suffering from septicemia comprises  
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
PT supplement endogenous PAF-AH activity and to inactivate pathological  
PT amounts of PAF

XX Claim 1: Column 47-50; 54pp; English.

PS The present sequence is human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH) protein.

CC The invention relates to human plasma platelet-activating factor  
CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
CC invention also relates to method of treating a mammal susceptible to  
CC or suffering from septicemia. PAF functions in normal physiological  
CC processes such as inflammation, haemostasis and parturition. PAF-AH  
CC specific antibodies are used in the diagnostic methods to detect abnormal  
CC levels of PAF-AH in serum and also for treating the pathological  
CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
CC shock and arthritis. PAF-AH antibody is also useful for screening a  
CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
CC replacement of nucleotide G to T at position 996 within exon 9 resulting  
CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human  
CC plasma PAF-AH gene.

XX Sequence 441 AA;

alignment\_scores:

Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x AAE00761

Align seg 1/1 to: AAE00761 from: 1 to: 441

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1 MetValProProLysLeuHisValLeuPheCysLeuGlyCysLeuAl 17  
88 TGTGTTTTATCCTCTTTGCTGCAATACATAAATCCTGTGCCCATGA 137  
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17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
138 AATCATCAGCTGCTGCTCAACAAATACAGTACTGCTGCTGCTGCAAGC 187  
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34 ySerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
188 TTTGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCCTGTTGTTG 237  
|||||  
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67  
238 TACAGACTTAATGTTGATCACACTTAATAAGGCACCTTCCTGCTTAT 287  
|||||  
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
288 ATTATCATCCCAAGATAATGATCGCTTTGACACCCCTTTGGATCCCAAT 337  
|||||  
84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
338 AAAGAATAATTTTGGGTCTTAGCAAAATCTCTGGAACACACTGCTTAT 387  
|||||  
101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117  
388 GGGCAACATTTTGAGGTTACTCTTTTGGTTCAATGACAACTCCTGCAACT 437  
|||||  
117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134  
438 GGAATTCCTCCTCGAGCCCTGCTGCAAAATATCCACTTGTGTTTCTCT 487  
|||||  
134 rPasnSerProLeuArgProGlyLysTrpProLeuValAlaPheSer 150  
488 CATGCTCTGGGGCATTGAGACACTTTTATCTGCTATTGGCATTGACCT 537  
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151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167  
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588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637  
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638 AAGTCTTTGGCTCTACCTTAGAACCTCAACAAAGAGAGGAGGACACATAT 687  
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201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluGluThrHisI 217  
688 ACGAAATGAGCAGGTAGCGCAAGAGCAAGAAAGTGTTCCTCAAGCTCTCA 737  
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217 eArgAsnGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234  
738 GTCTGATTCTTGACATTGATCATGGAAAGCCAGTGAAGAAATGCATTAGAT 787

38 ATGTGTGCACCCCAAATTCGATGTGCTTTTCTGCCTGTGCGGTGCCTGGC 87  
1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17  
88 TGTGGTTTATCCTTTTCGACTGGCAATACATAAATCCTGTGCCCATATGCA 137  
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34  
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51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyC 67  
238 TACAGACTTATGTTTCATCACAATAAGGCACCTTCCTGCGTTTAT 287  
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
288 ATTATCATCCCAAGATTAATGATGCCTTCACACCCCTTGGATCCCAAT 337  
84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100  
338 AAAGATAATTTTGGGTGCTTACCAAAATTTCTTGGACACACTGGCTTAT 387  
101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117  
388 GGGCAACATTTTGAGGTACTCTTGGTTGCTCAATGCACAACTCCGCAACT 437

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117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134
438 GGAATCCCTCTGAGCCTGGTGAATAATATCCATCTGTTCTTTCT 487
134 rPAsnSerProLeuArgProGlyGluLysIleValPheSer 150
488 CATGGCTCTGGGCATTCAGGACATTTATTCCTGATTGGCATTGACCT 537
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyLeuAspLe 167
538 GGCATCTCATGGGTTTATAGTTGCTGCTAGAACACAGACAGATAGCTG 587
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seq\_documentation\_block:

ID AAR71920 standard; Protein; 441 AA.

AC AAR71920;

DT 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant SI08A.

DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108

XX /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

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Quality: 2351.00

Length: 441

Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.546

alignment\_block:

US-09-922-067-9 x AAR71920

Align seg 1/1 to: AAR71920 from: 1 to: 441

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Mon Mar 11 10:02:12 2002

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us-09-922+067-9.rag

Page 20

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About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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: Sequence 8, Application US/08470187  
: Patent No. 5532152  
: GENERAL INFORMATION:  
: APPLICANT: Cousins, Lawrence S.  
: APPLICANT: Eberhardt, Christine E.  
: APPLICANT: Gray, Patrick W.  
: APPLICANT: Tjoelker, Larry W.  
: APPLICANT: Wilder, Cheryl L.  
: TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
: TITLE OF INVENTION: Hydrolase  
: NUMBER OF SEQUENCES: 11  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
: STREET: 6300 Sears Tower, 233 South Wacker Drive  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/470,187  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: No 5532152and, Greta E.  
: REGISTRATION NUMBER: 35,302  
: REFERENCE/DOCKET NUMBER: 31672  
: TELEPHONE: (312) 474-6300  
: TELEFAX: (312) 474-0448  
: TELEX: 25-3658  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 441 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
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seq documentation block:
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids

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TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-905-8

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Patent No. 5656431  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/483,232
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/318,905
: FILING DATE: 06-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/133,803
: FILING DATE: 06-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 565643land, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/32689
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3658
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 441 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-483-232-8

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seq_documentation_block:
: Sequence 8, Application US/08485938A
: Patent No. 5847088
: GENERAL INFORMATION:
: APPLICANT: Cousens, Lawrence S.
: APPLICANT: Eberhardt, Christine D.
: APPLICANT: Gray, Patrick W.
: APPLICANT: Le Trong, Hai
: APPLICANT: Tjoelker, Larry W.
: APPLICANT: Wilder, Cheryl L.
: TITLE OF INVENTION: Platelet-Activating Factor
: TITLE OF INVENTION: Acetylhydrolase
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,938A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/318,905
: FILING DATE: 06-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/133,803
: FILING DATE: 06-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5847088and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 278666/32792
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3658
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 441 amino acids

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: Patent No. 5977308
: GENERAL INFORMATION:
: APPLICANT: Cousens, Lawrence S.
: APPLICANT: Eberhardt, Christine D.
: APPLICANT: Gray, Patrick W.
: APPLICANT: Le Trong, Hai
: APPLICANT: Tjoelker, Larry W.
: APPLICANT: Wilder, Cheryl L.
: TITLE OF INVENTION: platelet-Activating Factor
: TITLE OF INVENTION: Acetylhydrolase
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
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seq\_documentation\_block:

; Sequence 8, Application US/09328474  
; Patent No. 6045794

; GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.

; APPLICANT: Gray, Patrick W.

; APPLICANT: Le Trong, Hai

; APPLICANT: Tjoelker, Larry W.

; APPLICANT: Wilder, Cheryl L.

; TITLE OF INVENTION: Platelet-Activating Factor

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/328,474

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/483,232

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905

; FILING DATE: 06-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,803

; FILING DATE: 06-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Rin-Laures, Li-Hsien

; REGISTRATION NUMBER: 33,547

; REFERENCE/DOCKET NUMBER: 27866/34026

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3658

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 441 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

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Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

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; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
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; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 6098836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-100-546-8

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    Quality: 2354.00      Length: 441
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; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.

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; Patent No. 6203790  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/577,758  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/010,715  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6203790and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32793  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-577-758-8

alignment\_scores:  
Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 99.773  
alignment\_block:  
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: GENERAL INFORMATION:
: APPLICANT: Consens, Lawrence S.
: APPLICANT: Eberhardt, Christine D.
: APPLICANT: Gray, Patrick W.
: APPLICANT: Le Trong, Hai
: APPLICANT: Tjoelker, Larry W.
: APPLICANT: Wilder, Cheryl L.
: TITLE OF INVENTION: Platelet-Activating Factor
: TITLE OF INVENTION: Acetylhydrolase
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,938A
: FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/318,905
: FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/133,803
: FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
: NAME: No. 5847088and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3658
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-485-938A-33

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Quality: 1954.50 Length: 442
Ratio: 4.677 Gaps: 1
Percent Similarity: 95.023 Percent Identity: 82.353

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Align seg 1/1 to: US-08-485-938A-33 from: 1 to: 444

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seq\_documentation\_block:

; Sequence 28, Application US/08483140

; Patent No. 5698403  
; GENERAL INFORMATION:  
; APPLICANT: ICOS Corporation  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,140  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 6-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5698403and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32781  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 444 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-483-140-28  
  
alignment\_scores:  
Quality: 1935.50 Length: 442  
Ratio: 4.686 Gaps: 1  
Percent Similarity: 93.439 Percent Identity: 80.769  
  
alignment\_block:  
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seq\_name: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:us-08-485-938A-32  
seq\_documentation\_block:  
; Sequence 32, Application US/08485938A  
; Patent No. 5847088  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Morun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,938A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5847088and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32792  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 444 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-938A-32

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7 / FILING DATE: 0 OCT 1994  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-27

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    Ratio: 4.031          Gaps: 2
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Align seg 1/1 to: US-08-483-140-27 from: 1 to: 440

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APPLICANT: Le Trong, Hai  
 APPLICANT: Tjoelker, Larry W.  
 APPLICANT: Wilder, Cheryl L.  
 TITLE OF INVENTION: Platelet-Activating Factor  
 TITLE OF INVENTION: Acetylhydrolase  
 NUMBER OF SEQUENCES: 36  
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 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
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 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-8402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
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 REFERENCE/DOCKET NUMBER: 27866/32792  
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 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3658  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 440 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-485-938A-31

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 Ratio: 4.031 Gaps: 2  
 Percent Similarity: 85.068 Percent Identity: 66.516

## alignment\_block:

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 738 GTCTGATTTCTTGACATTCATGCAAGCCAGTGGAAGATGCAATGATAGAT 787  
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 233 erAlaIleLeuAspIleGluHisGlyAspProLysGluAsnValGluGly 249  
 788 TTAAGTTTGTATGGAACAACACTGAGGACTCTATTGATAGGGGAAAAAT 837  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 250 SerAlaPheAspMetLysGlnLeuLysAspAlaIleAspGluThrLysII 266  
 838 AGCAGTAAATGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTA 887  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 266 eAlaLeuMetGlyHisSerPheGlyGlyAlaThrValLeuGlnAlaLeuS 283  
 888 GTGAAGATCAGAGATTCAGATGCTGTTGCTGCTGATGCGATGCTGCTTT 937  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 283 erGluAspGlnArgPheArgCysGlyValAlaLeuAspProTrpMetLys 299  
 938 CCATCTGGAATATTTTCAATATCTGCTTAATATCATAAATAATGAAAAAT 1037  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 316 eAsnSerAlaLysPheGlnThrProLysAspIleAlaLysMetLysLysP 333  
 1038 GCTACTCACCTGATAAAGAAAGAAAGAT.GATTACAATCAGGGGTTTCAGT 1086  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 333 heTy:GlnProAspLysGluArgLysAsnAspTy:AsnGlnGlyLeuArg 349  
 1087 CCACGAGAATTTTCTGCTACTTCACTTTGCAACTGCGCAAAATATATGGAC 1136  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 350 .HisGlnAsnPheAspAspPheThrPheValThrGlyLysIleIleGlyA 366  
 1137 ACATGCTCAAAATTAAGGGGACACATAGTCAATGACGCTATTGATCTT 1186  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 366 snLysLeuThrLeuLysGlyGluIleAspSerArgValAlaIleAspLeu 382



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1187 AGCAACAACCTTCATTAGCATCTCTACAAAAGCAATTTAGGACTTCATAA 1236
    ::::::::::::::::::::::::::::::::::::::::::::::::::::
383 ThrAsnLysAlaSerMetAlaPheLeuGlnLysHisLeuGlyLeuGlnCly 399
1237 AGATTTTGATCAGTGGGACTGCTTGATTCAAGGAGATGATGAGAAATCTTA 1286
    ::::::::::::::::::::::::::::::::::::::::::::::::::::
399 sAspPheAspGlnTyrAspProLeuValGlnGlyAspAspGluAsnLeuI 416
1287 TTCAGGACCAACATTACACACCAATCAACACATCATGTTACAGAAC 1336
    ::::::::::::::::::::::::::::::::::::::::::::::::::::
416 leProGlySerProPheAspAlaValThrGlnAlaProAlaGlnGlnHis 432
1337 TCTTCAGGAATAGAGAAATACAAAT 1360
    ::::::::::::::
433 SerProGlySerGlnThrGlnAsn 440
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OM of: US-09-922-067-9 to: PIR\_68.\* out\_format : pfs

Date: Mar 9, 2002 12:25 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=framer\_n2p.model; -DEV=xlp  
-Q/cgu2\_1/usPT0.spool/US09922067/runat\_07032002\_140445\_9311/app\_query.fasta\_1.1439  
-DB=PIR\_68 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -CGAPOP=4.500  
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DFLOP=6.000  
-DELEXT=7.000 -START=1 -NATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=2000000000 -USER=US09922067 -CGNI\_1\_79 -NCPU=6 -ICPU=3  
-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-922-067-9

Query length: 1361

Database: PIR\_68.\*

Database sequences: 219241

Database length: 76174552

Search time (sec): 96.640000

seq\_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
pir2:S60247	+	2354.00	3563.20	4.0e-191	441	platelet-activating factor-act
pir2:JC5021	+	1572.50	2376.21	5.3e-125	436	platelet-activating factor-act
pir2:T32756	+	497.00	743.65	5.1e-34	384	hypothetical protein W03B9.6
pir2:T28936	+	493.50	736.48	1.0e-33	476	hypothetical protein CS2B9.7
pir2:T39268	+	295.50	436.44	5.8e-17	438	hypothetical protein SP2106.11
pir2:G83740	+	245.50	366.34	4.6e-13	450	hypothetical protein BH0727 [im
pir2:D83408	+	162.50	232.52	1.1e-05	546	hypothetical protein PA1907 [im
pir2:T36311	+	149.00	214.89	0.0002	391	probable lipase - Streptomyces
pir2:F82958	+	148.50	208.03	0.0002	795	dipeptidyl-peptidase XF0015 [im
pir2:JND490	+	120.50	173.59	0.0360	310	28k lipase precursor - Streptom
pir2:S75452	+	119.00	165.33	0.0518	622	hypothetical protein slr1506 -
pir2:D75217	+	112.00	161.37	0.1871	286	probable 2'-acetyl-1-alkylglycer
pir2:S66261	+	110.50	151.27	0.2751	711	X-Pro dipeptidyl-peptidase (EC
pir2:F71174	+	110.00	151.66	0.2991	622	hypothetical protein PH0594 - E
pir2:T36421	+	108.50	154.93	0.3750	326	hypothetical protein SCF34.22 -
pir2:S19172	+	107.00	151.63	0.5084	367	cytochrome P450 2B4 - rat (freq
pir2:A85511	+	106.50	153.36	0.5442	275	acyltransferase family (importe
pir2:C72111	+	106.50	153.36	0.5442	275	diene-lactone hydrolase family
pir2:E75057	+	106.00	145.44	0.6531	632	peptidase PAB1418 - Pyrococcus
pir2:G82193	+	104.50	140.44	0.9036	868	aminopeptidase N VC1494 [impor
pir2:A49737	+	103.50	138.32	1.11	931	dipeptidyl aminopeptidase (EC
pir2:F84914	+	103.50	138.10	1.11	955	hypothetical protein At2g47390
pir2:D81302	+	102.00	139.99	1.41	588	probable ATP/GTP-binding prote
pir2:T15247	+	100.00	138.80	2.04	474	hypothetical protein T05E7.1 -
pir2:T41703	+	100.00	134.38	2.15	793	dipeptidyl aminopeptidase - fil
pir2:T09499	+	99.50	131.54	2.43	1010	ATP-dependent clip proteinase
pir2:C82418	+	98.00	133.36	3.10	627	GGDEF family protein VCA0785 [i
pir2:S70481	+	97.50	133.92	3.37	538	hypothetical protein - Synchoc
pir2:A84693	+	97.50	128.91	3.57	964	hypothetical protein At2g29190
pir2:T25621	+	97.50	128.83	3.57	972	hypothetical protein C37H5.2 -
pir2:A48592	+	96.50	129.46	4.23	757	transferrin receptor protein -
pir2:H71947	+	96.00	131.59	4.51	541	arginine-tRNA ligase (EC 6.1.1
pir2:C82490	+	95.50	136.49	4.65	280	probable potassium channel prot
pir2:A43828	+	95.50	126.91	5.21	854	3',5'-cyclic-GMP phosphodiester
pir2:B34089	+	95.00	130.02	5.48	544	carboxylesterase (EC 3.1.1.1)
pir2:A71556	+	95.00	129.64	5.51	569	probable S1 ribosomal protein -
pir2:S38060	+	95.00	128.96	5.55	616	carboxylic acid transport prote
pir2:C71554	+	94.50	122.92	6.52	1138	probable transmembrane protein
pir2:T52523	+	94.50	122.40	6.56	1209	hypothetical protein B3J23.190
pir2:JX0096	+	94.00	133.26	6.30	313	lectin precursor, fucose-specifi

pir2:E96803 + 93.00 130.02 7.81 382 ! probable lipase, 4162-5963 [im  
pir2:T34457 + 93.00 127.16 8.08 533 ! hypothetical protein T19h12  
pir2:G41426 + 93.00 126.99 8.09 544 ! carboxylesterase (EC 3.1.1.1)  
pir2:G84601 + 93.00 122.94 8.49 871 ! probable protein kinase [im

seq\_name: pir2:S60247

seq\_documentation\_block:

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Tjosioiker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U0157; NID:g780132; PIDN:AAC50126.1; PID:g780133

alignment\_scores:

Quality: 2354.00

Ratio: 5.338

Percent Similarity: 100.000

Percent Identity: 99.773

alignment\_block:

US-09-922-067-9 x S60247

Align seg 1/1 to: S60247 from: 1 to: 441

38 ATGGTCCGCCCAAAATTCGATGCTTTCTGCTGGGCTGCTGCG 87  
1 MetValProLysLeuHisValLeuPheCysLeuGlyCysLeuAl 17  
88 TGTGGTTATCTCTTTCAGCTGGCAATACATAATCTGTGGCCCATAGA 137  
17 aValValtyrProPheAspPrpGlnTyrIleAsnProValAlaHisMetL 34  
138 AATCATCAGATGGGTCAACAAATACAGTACTGATGCTGCTGCAAGC 187  
34 YsserSerAlaIrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
188 TTGGGCCAAACTAAATPCCCGGGGAAATGGGCTTATTCGCTGGTTG 237  
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67  
238 TACAGACTTAATGTTTGATCACACTAATAAGGCGACCTTCTTTCGCTTAT 287  
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84  
288 ATTATCATCCCAAGATATGATGCTGCTGACACCTTTGGATGCCAAAT 337  
84 YrTyrProSerGlnAspAsnArgLeuAspThrLeuTrpIleProAsn 100  
338 AACAATATTTTGGGGTCTTAGCAATTTCTTGGAAACACACTGGCTTAT 387  
101 LysGlnTyrPheIrpGlyLeuSerLysPheLeuGlyThrHisrPleuMe 117  
388 GGGCAACATTTTGGGTTACTCTTGGTTCATATGACAACTCTGCAAACT 437  
117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134  
438 GGAATTCCTCTGAGCGCTTGTGAAATAATATCATCTTGTGTTTTCT 487  
134 rPasnSerProLeuArgProGlyLysTyrProLeuValValPheSer 150  
488 CATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCATTCAC 537  
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyLeuAsp 167

538 GGCATCTCATGGTTTATGCTGCTAGAACACAGAGATGATCTG 587  
|||||  
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspSerA 184  
588 CATCTGGCAACTTACTATTTCAGACCAATCTGCTGAGAAATAGGGAC 637  
|||||  
184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200  
638 AAGTCTTGGCTCTACCTTAGAACCTGAAACAAAGAGAGGAGACACATAT 687  
|||||  
201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217  
688 ACGAAATGACCGGTAGCGCAAGACGAAAGAAATGTTCCCAAGCTCTCA 737  
217 eaRAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234  
738 GTCGTGATCTTGACATGATCATGAGGAGCCAGTGAAGATGATTAGAT 787  
234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250  
788 TTAAGTTTCATATGAACAACTGAAGACTCTATTGATAGGAAATAAT 837  
|||||  
251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267  
838 AGCAGTAATTTGGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTA 887  
267 eaLaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284  
888 GTGAAGATCATGACATTCAGATGCTGTTATTCCTGCTGATCATGATGTTT 937  
284 erGluAspGlnAlaGpPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300  
938 CCACCTGGTGATGAAGATATATTCAGAAATTCCTCAGCCCTCTTTTAT 987  
301 ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheI 317  
988 CAACCTCGAATATTTCCATATTCCTGCTAATATCATATAAATGAAAAAT 1037  
317 eaSnSerGluTyrPheGluTyrProAlaAsnIleLysMetLysLysC 334  
1038 GCTACTCACCTGATTAAGAAAGAAAGATGATTACAAATCAGGGGTTTCAGTC 1087  
334 ystYrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 1088  
1088 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATTAATGGACA 1137  
351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHI 367  
1138 CATGCTCAATTAAGGGAGACATAGATTCAAATCAGCTATTGATCTTA 1187  
367 smetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384  
1188 GCAACAAAGCTTCATTAGCATCTTACAAAAGCATTTAGGACTTCATAAA 1237  
384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400  
1238 GATTTTGATCAGTGGAGCTGCTGATTGAAAGAGATGATGAGATCTTAT 1287  
401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuI 417  
1288 TCCAGGGACCAACATTAACACAAACCAATCAACACATCATGTTTACAGAACT 1337  
417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434  
1338 CTTACAGGAATAGAAATACAAAT 1360  
434 erSerGlyIleGluLysTyrAsn 441

seq\_name: p1r2:JC5021

seq\_documentation\_block:

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase  
C:Species: *Capra porcellus* (guinea pig)  
C>Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000  
C:Accession: JC5021; PC4207  
R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.;  
J. Biochem. 120, 838-844, 1996  
A:Title: Cloning, expression and characterization of plasma platelet-activating f  
A:Reference number: JC5021; MUID:97103479  
A:Accession: JC5021  
A:Molecule type: DNA  
A:Residues: 1-436 <KARL>  
A:Cross-references: DDBJ:D67037; NID:gl644228; PIDN:BAAL1054.1; PID:gl644229  
A:Accession: PC4207  
A:Molecule type: protein  
A:Residues: 123-129,134-139,208-217,258-264;332-337;341-345;346-361;373-384;385-3  
A:Experimental source: liver  
A:Comment: This enzyme converts platelet-activating factor to an inactive metabol  
C:Keywords: glycoprotein; hydrolase  
F:1-21/Domaig: signal sequence #status predicted <SIG>  
F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <M  
F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

## alignment\_scores:

Quality: 1572.50 Length: 441  
Ratio: 4.022 Gaps: 2  
Percent Similarity: 88.662 Percent Identity: 66.213

## alignment\_block:

US-09-922-067-9 x JC5021

Align seg 1/1 to: JC5021 from: 1 to: 436

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|||||  
1 MetAlaProLysLeuHisThrLeuPheCysLeuSerGlyPheLeuAl 17  
88 TGTGGTTTATCTCTTTCACATGCGCAATACATAAATCTCTGTTGCCCATATGA 137  
|||||  
17 aLeuValHisProPheAspTrpArgAspLeuAspProValThrTyrIleG 34  
138 AATCATCAGCATGGTCAACAAATACAACTACTGATGGCTGCTGCAAGC 187  
|||||  
34 InSerValTrpIleGlnArgIleGlnSerGluLeuLeuIleThrSer 50  
188 TTTGGCCAACTAAATCCCGGGGAAATGGCCCTATTTCGTTGCTGGTGG 237  
|||||  
51 PheGlyHisThrThrIleProLysGlyAsnGlyProTyrSerValGlyCy 67  
238 TACAGACTTAATGTTTATGATCACACTAATAAGGCGCACCTTCCTTCGCTTAT 287  
|||||  
67 sThrAspLeuMetSerGlyTyrThrAsnGlnSerPheLeuArgLeu 84  
288 ATTATCCATCCCAAGATAATGATGCGCTTTGACACCCCTTTGGATCCCAAT 337  
|||||  
84 yTyrProSerGlnAspAsnAspPheProAspAlaLeuTrpIleProAsn 100  
338 AAGAATAATTTTGGGGTCTTAGCAAAATTTCTTGGAAACACACTGGCTTAT 387  
|||||  
101 GluGluTyrPheGlnGlyLeuThrGluThrLeuGlyAlaSerSerPheLe 117  
388 GGGCAACATTTTGAGTTACTCTTGGTTCAATGACAACTCCTGCAAACT 437  
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117 uGlyLysLeuLeuLysLeuLeuTyrGlySerValLysValProAlaLys 134  
438 GGAATTCCTCCTCTGAGGCTGGTGAATAATATCCACTTGTGTTTCTTCT 487  
|||||  
134 rPAsnSerProLeuLysThrGlyGluLysTyrProLeuIleIlePheSer 150  
488 CATGCTCTTGGGGCATTCAGGACACTTTATTCTGCTATTGGCATTGACCT 537  
|||||  
151 HisGlyLeuGlyAlaPheArgSerIleTyrSerAlaIleGlyIleGluLe 167

538 GCATCTCATGGGTTTATAGTCTGCTGTAGACACAGACATAGATCTG 587  
167 uAlaSerHisGlyPheIleValAlaIaValAlaGluHisArgAspGluSerA 184  
588 CATCTGCAACTTACTATTTCAGGACCAATCTGTCAGAAATAGGGAC 637  
184 laAlaAlaThrTyrPheGlnAspAlaProAlaAlaGluSerGlyAsn 200  
638 AGTCTTGGCTCTACCTTAGAACCTTGAACAGACAGAGGAGACATAT 687  
201 ArgSerTrpIleTyrTyrLysVal.....GlyAsnLeuGluThrGlu 215  
688 ACCAATGAGCAGGTACGGCAAGACAAAGAAATGTTCCCAAGCTCTCA 737  
215 uArgLysArgGlnLeuArgGlnArgGlyGluGluCysSerGlnAlaLeu 232  
738 GTCTGATCTTGCATCATCATGCAAGCCAGTGAAGATGCATTAGAT 787  
232 erTrpLeuSerIleAspGluGluProValLysAsnValLeuAsp 248  
788 TTAAGTTTGATATGACAACTGAAGACTCTATTGATAGGCAAAAT 837  
249 LeuAsnPheAspIleGlnLeuLysGlySerLeuAspArgSerLysVa 265  
838 AGCAGTAATTGACATCTCTTGTGTGGAGCAACGGTTATTTCACACTCTTA 887  
265 lAlaIleIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeu 282  
888 GTGAAGATCAGAGATTCAGATCTGCTATGTCCTGGATGCATGATGTT 937  
282 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspProTrpMetPhe 298  
938 CCATCGGGTGAGTAGATATATCCAGATCTCTCAGCCCTCTTTTTAT 987  
299 ProValGlyGluAspValHisSerLysIleProGlnProLeuPheIle 315  
988 CCACTCTGAATATTTCCAATATCTCTGCTTAATATCAATAAATAAAT 1037  
315 eaSnSerGluTyrPheGlnSerAlaAsnAspThrLysLysIleGluLysP 332  
1038 GCTACTCCTCATTAAGAAACAAGATGATTACAATCAGGGTTCAGTC 1087  
332 heTyrGlnProGlnLysGluArgLysMetIleAlaValLysGlySerVal 348  
1088 CACCAAGATTTTGTGACTTCACTTTGCCAAGTGGCAAAATATTTGACA 1137  
349 HisHisAsnPheValAspPheThrPheAlaThrGlyLysIleIleGly 365  
1138 CATGCTCAATTAAGGGAGACATAGATTCAAAATGSCAGCTATTGATCTTA 1187  
365 nMetCysLeuLysGlyLysIleAspSerGluValAlaMetAspLeu 382  
1188 GCAACAAGCTTCATTAGCATTTCTTACAAAAGCAATTTAGACTTCATAAA 1237  
382 LeAsnLysAlaSerLeuAlaPheLeuGlnLysTyrLeuGlyLeuAsp 398  
1238 GATTTTGTGACTGGGACTGCTTGTGATGAAGCAGATGATGAGATCTTAT 1287  
398 AsnPheAspGlnTrpAsnSerLeuMetGluGlyAspGluAsnLeuIle 415  
1288 TCCAGGGACCAACATTAACCAACCAATCAACACATCATGTTTACAGAACT 1337  
415 eProGluPheThrIleProThr.....MetGlnSerS 427  
1338 CTTCAGGAATAGAAATACAT 1360  
427 erThrGlyThrGluGlnArgAsn 434

seq\_name: pir2:T32756

seq\_documentation\_block:  
hypothetical protein W03G9.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T32756  
R:Dance, M.; Keppler, D.  
A:Description: The sequence of C. elegans cosmid W03G9.  
A:Reference number: 221220  
A:Accession: T32756  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-384 <DAN>  
A:Cross-references: EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN00019; CESP:W03G9.6  
A:Experimental source: strain Bristol N2; clone W03G9  
C:Genetics:  
A:Gene: CESP:W03G9.6  
A:Map position: 1  
A:Introns: 47/3; 90/2; 142/2; 183/3; 333/3

alignment\_scores:  
Quality: 497.00 Length: 348  
Ratio: 2.097 Gaps: 9  
Percent Similarity: 68.103 Percent Identity: 33.908

alignment\_block:

US-09-922-067-9 x T32756 ..

Align seg 1/1 to: T32756 from: 1 to: 384

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14 LysMetPro.....GlyInPheLysValIglyCysMetAspLeuMe 27  
250 GTTGTGATCAC...ACTAATAAGGGACACTTCTTTCGCTTATATATPCCAT 296  
27 lIleGluGluAlaIleGlySerGlyLeuPheMetArgLeuPheProT 44  
297 CCCAAGATATGATCGCCTTGAC.....ACCTTTGGATCCCA 334  
44 hr...AspSerGluIleThrGlyProSerSerLeuProValTrpIlePro 59  
335 AATAAAGAATATTTTGGGGTCTTAGCAAAATTTCTTGA...ACACACTG 381  
60 ArgProGluTyrAlaTyrGlyValGlyGlyLeuGlyHisSerProH 76  
382 GCTTATGGGCAACATTTTGAGCTTACTCTTTGGTTCAATGACAACTCTTG 431  
76 sGlnMetAspLeuIleSerSerLeuValIleGlyAspLysArgValAspC 93  
432 CAAACTGGAATTCCTCTCTG...AGGCTGCTGTAATAATATCCACTTGT 478  
93 yIleAspAsnAlaGlnLeuSerThrLysSerAspLysTrpProValLeu 109  
479 GTTTTTTCTCATGCTCTTGGGCAFTTCAGCAGACTTTATTCGCTATTGG 528  
110 ValPheSerHisGlyLeuGlyGlySerArgThrPheTyrSerThrTyrCy 126  
529 CATTCACCTGGCATCTCATGGTATTATAGTTGCTGTGTAAGACACAGAG 578  
126 sThrSerLeuAlaSerHisGlyTyrValValAlaAlaValGluHisArg 143  
579 ATAGATTCGATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAA 628  
143 spSerSerAlaCysTrpThrTyrLysLeuValGluLysAsnGlyThrLeu 159  
629 ATAGGGGACAAGTCTTGCTCTACCTTAGAACCTTGAACCAAGAGGAGGA 678  
160 ValGluLysProMetLysIleLeuLysValAspArgAsnAspLysAspG 176  
679 GACACATATACGAATGAGCAGGTACGGCAAGAGCAAGAAAGATGTCCT 728  
176 nPheLysIleArgAsnGluInValGlyLysArgAlaGluGluCysAla 193  
729 AAGCTCTCAGTCTGATTCTTGCATTTGACATTTGATCATGAAAGCCAGTGAAGAAT 778

```

193 ysAlaValLysIleLeuGluGlnLeuAspSerGlyAsn...ValLysAsp 208
779 GCATTAGATTTA.....AGTTTGATATGGAACAACACTGAAGGACTCTAT 822
209 LysValIleIleGlyAsnAsnAlaAsnLeuGluPhePheLysAsnLysLe 225
823 TGATAGGGAATAATAGCAGTAATTCGACATCTTTTGGTGGAGCAACGG 872
225 uLeuThrThrAlaSerIleIleGlyHisSerPheGlyGlyAlaThrS 242
873 TTATTACAGACTCTTACTGAGAGACAGAGATTAGATGCTGGTATTGCCCTG 922
242 erIleAlaSerSerSerAsp.....PheGlnLysAlaIleValLeu 256
923 GATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAAATCCCTCA 972
257 AspGlyTrpMetTyrProLeuAspGlnAsnGlnGlnGluAlaLysG 273
973 GCCCTCTTTTATCAACTCTGAATATTTCGAATATCTGCTAATATCA 1022
273 nProIleMetPheLeuAsnValGlyAspTrpGlnTrpAsnGluAsnLeuG 290
1023 TAAAAATGAAAATGCTACTCACCTGATATAAAGAAAGAGATGATTACA 1072
290 luValMetArgLysIleLeuProAsnAsnGluGlyAsnIleLeuLeuThr 306
1073 ATCAGGGCTTCAGTCACCAGAAATTTGCTGACTTCACATTTTGGCACTGG 1122
307 LeuSerGlyAlaValHisGlnSerPheThrAspPheProPheValPhePr 323
1123 CAAAATATGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAAATG 1172
323 oAsnTrpLeuAlaLysGlnPheGlyValHisGlyProThrGluProTyrL 340
1173 CAGCTATTGATCTTACCAACAAGCTTCATTAGCATCTTACAA 1216
340 eucysMetGlnSerAlaIleGluLeuThrLeuSerPheLeuLys 354
seq_name: pir2.T28936
seq_documentation_block:
hypochemical protein C52B9.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28936
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: Z20345
A:Accession: T28936
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-476 <NFI>
A:Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN00028; CESP:C52B9.7
A:Experimental source: strain Bristol N2; clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.7
A:Map position: X
A:Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

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alignment_scores:
Quality: 493.50      Length: 383
Ratio: 2.127        Gaps: 8
Percent Similarity: 60.574      Percent Identity: 32.115

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alignment_block:
US-09-922-067-9 x T28936

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Align seg 1/1 to: T28936 from: 1 to: 476

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146 GCATGGGTCACAAATACAAAGTACTGCTGCTGCAAGCTTTGGCCA 195

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```

75 SerTyrIleSerSerProGlnValLeuThrArgGlnValSer..... 88
196 AACTAAAATCCCGGGGAAATGGCCCTTATTCCGTTGGTTGGTGTACAGACT 245
89 .....GlyGlnPheGlnValGlyCysLysAspL 98
246 TAATGTTTGATCACACT.....ATAAGGCACCTCTCTTCGCTTTA 286
98 euMetIleAspGlyThrValLeuGlyAspArgGlyLeuPheMetArgLeu 114
287 TATTATCCATCCCAAGATAATGATCGCCTTGAC.....ACCT 324
115 TyrPheProThr...AspSerGlnAlaAlaAspIleSerSerTyrProLe 130
325 TTGGATCCCAATAAAGAAATATTTTCCGGTCTTTAGCAAAATTTCTTGGGA 373
130 utrPLeuProLysProGlnTyrAlaHisGlyLeuGlyGluTyrLeuGlyG 147
374 ..ACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAATG 421
147 InSerSerGlnLysMetAsnValIleThrSerThrValValGlyGluLys 163
422 ACAACTCTCGCAACTGGAATTCCTCTCTCAGGCGCTGT...GAAAAATA 468
164 ArgGluAspCysIleGluAsnAlaGlnMetSerThrLysCysAspLysTr 180
469 TCACACTTGTGTTTCTCATGCTCTTGGGGCATTCAGACACTTTATT 518
180 pProIleValValPheSerHisGlyLeuGlyGlySerArgThrPheTyrS 197
519 CTGCTATTGGCATTGACCTCGCATCTCAGGGTTTATAGTGTGCTGTGTA 568
197 erThrTyrCysThrSerLeuAlaSerHisGlyTyrValValAlaAlaVal 213
569 GAACAC..... 574
214 GluHisLysTrpGlyLysSerGlyGlyArgCysAspHisValAlaPheSe 230
575 ...AGAGATAGATCTGCATCTCGCAACTTACTATTTCAGGACCAATCTG 620
230 rCysArgAspHisSerAlaCysTrpThrTyrGlnLeuThrGluLysAsnG 247
621 CTCGCAAAATAGGGGACAACTGTCCTCTACCTTAGAACCCCTGGAACAA 670
247 IyGluLeuValGluGlnProIleLysIleLysLeuIleGluLysAsnGlu 263
671 GAGGAGGAGACACATATAGCAATGAGCAGCTACGGCAAGAGACAAAGA 720
264 LysAsnGluPheLysIleArgAsnGlnGlnValGlyLysArgValThrGl 280
721 ATGTTTCCCAAGCTCTCAGTCTGATCTTTCATGATGATCATGGAAG...C 767
280 uCysValLysAlaLeuAsnValLeuGluGlnLeuAsnLeuGlyThrValP 297
768 CAGTGAAGAATGCTATAGATTTTAAAGTTTGATATGCAACAACCTGAAGGAC 817
297 roGluLysValLeuIleGlyAsnAspTyrAsnTrpAlaGlnPheLysAsn 313
818 TCTATTGATAGGCAAAAATAGCAGTAATTCAGACTCTTTTGGTGGAGC 867
314 LysLeuValMetSerSerAlaSerValIleGlyHisSerPheGlyGlyAl 330
868 AACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTCAGATCTGCTATTG 917
330 aThrSerLeuAlaSerSerAlaTyrThrThrAspPheGlnLysAlaIleV 347
918 CCTGGATGCTGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 967
347 alPheAspGlyTrpMetTyrProLeuAspSerThrGlnGlnGluGlnAla 363
968 CUTCAGGCCCTCTCTTTTATCAACTCTGAAATATTTCCAAATATCTCTGCTAA 1017
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[illegible]

seq\_documentation\_block:  
hypothetical protein SPBC106.11c - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T39268  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.  
submitted to the EMBL Data Library, August 1999  
A:Reference number: Z21840  
A:Accession: T39268  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-438 <L>  
A:Cross-references: EMBL:AL10295; PTDN:CA853727.1; GSPDB:SPBC106  
A:Experimental source: strain 972h-; cosmid c106

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alignment_scores:
  Quality: 295.50      Length: 452
  Ratio: 1.274        Gaps: 22
  Percent Similarity: 51.327    Percent Identity: 24.779

alignment_block:
  US-09-922-067-9 x T39268 ..

  Align seg 1/1 to: T39268 from: 1 to: 438

200 AARATCCCGCGGGAATGGCCCTTATTCGGTTGGT..... 235
   : : : : : | | | | | | | | | | | | | | | |
10 GlnLeuProAlaIyrCysGlyProLeuProValGlySerLeuValLeuG1 26
   .. : : : : : : : : : : : : : : : : : : : : :
236 .....TGTACAGACTTAATGTTTGGATCACA 260
   : : : : : | | | | | : : : : : | |
26 uLeuServalProGluGluPheArgCysGluTyrIsthrlleGluHisL 43
   : : : : : : : : : : : : : : : : : : : : :
261 CTAATAAGGCACCTTCTTCGCGTTATATATAT.....CCATCCCAA 301
   : : : : : | | | | | : : : : : | | | | | :
43 ysLeuArgThrValIysValargIlePheTyrProLeuAspProThrIys 59
   : : : : : : : : : : : : : : : : : : : : :
302 GAT...AATGATCGCCTTGGACACCCCTTGGATCCCAATAAAGAATATT 348
   : : : : : | | | | | | | | | | | | | | | |
60 AspValGluProArgThrAspGluLeuTyrPheHisGluGlyI1 76
   : : : : : : : : : : : : : : : : : : : : :
349 TTGGGGTCCTAGCAAAATCTTCGACACACACTGGCCTTAGGGCAACAATT 398
   : : : : : | | | | | | | | | | | | | | | |
76 eProGluValAlaIys.....GlyPheArgIrrTrp.....LeuL 88
   : : : : : : : : : : : : : : : : : : : : :
399 TGAGGTACTCTTTGGTTCAATCAGCAACTCTCGCAAACTGGAATTTCCOCT 448
   | | | | | PheAlaIysSerGlyLeuThr.....AsnLeuAlaLeuPro 101
   | | | | | : : : : : : : : : : : : : : : :
88 euArgAlaPheAlaIysSerGlyLeuThr.....AsnLeuAlaLeuPro 101

```

449 CTGAGGCGCTGGTGA .....AATATCCACT 474  
::: ||||| |||||  
102 ValTyrLysGlyGluLeuPheHisProProAsnAsnGlyLeuProVa 118  
475 TGTGTGTTTTTCTCATGCTTGGGCGATTTCAGACACACTTATCTGCTA 524  
::: ||||| |||||  
118 lPheIlePheSerHisGlyLeuValGlySerArgAsnValTyrSerSerL 135  
525 TTGGCATTGACCTGGGATCATTGCGTTTATAGTTTCTGCTGTAGAACAC 574  
::: ||||| |||||  
135 euCysGlyThrIleAlaSerTyrGlyIleValValLeuAlaMetGluHis 151  
575 AGAGATAGATCTGCA ..... 589  
152 ArgAspAsnSerAlaIleIleSerThrValArgAspProLeuHisProGl 168  
590 .TCGTCGAACCTTACTATTTCAGGACCAATCTGTCGAGAATAAGGGACAC 638  
168 uGluProProTyrValValGlnTyrArg .....GluIleSerAsp. 181  
639 AGTCTGGCTCTACTTTAGAACCTCGAAACAGAGGAGGAGACACATATA 688  
182 .....PheTyrAlaAspAlaThrValValLeu 190  
689 CGAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAG 738  
::: ||||| |||||  
191 GlnAsnGluArgLeuPheArgGlnGlnGluIleGlnIleAlaLeuGl 207  
739 TCTGATTCTTGACATT ..GATCATGGAAAGCCAGTGAAGAAT ..... 778  
207 nMetIleArgAsnIleAsnAspLeuGlyThrProAspGluAsnLeuProp 224  
779 .....GCATTTAGATTAAAGTTT .....GATATGGAAACAACCTG 811  
224 heLeuCysSerValAspSerPheTyrAsnSerValPheGlnSerMet 240  
812 AAGCAGCTTATTGAT .....AGGGAAAAAATAGCAGTAATTTGGACATTC 855  
||| ||||| |||||  
241 LysGlyAsnLeuAsnThrAlaGlnGlyLeuIleValAlaGlyHisSe 257  
856 TTTTGGTGGCAACGGTT .....ATTACAGACTC 884  
||||| ||||| |||||  
257 rPheGlyAlaAlaThrCysAlaPheIleSerGlySerSerThrLysSerL 274  
885 TTATGTAAGAT .....CAGAGATTAGATGTGTTATGCCCTG 922  
|| ||||| |||||  
274 euTyrAsnAspTyrMetPheHisThrGluPheLysCysSerIleLeuTyr 290  
923 GATCATGAGTCTTCACCTGGGTGAAGTATATTCAGAAATCTCTCA 972  
||| ||||| |||||  
291 AspIleTrpMetLeuProValArgGlnLeuHisLeuSerThrMetArgTy 307  
973 GCCC...CTCTTTTTTATCAACTCTGAATTTTCCAATATCTCGCTAATA 1019  
||| ||||| |||||  
307 rProThrLeuMetIleIleSerTyrGluPheArgArgPheValAspAsnP 324  
1020 TCATAAAATGAAAAATGCTAC ..... 1042  
::: ||||| |||||  
324 heGlnAlaLeuGluSerTrpLeuValAsnLysAspSerGluAsnGlnAsn 340  
1043 .....TCACCTGATAAGAAAGAAAGATGATTCAATCAGG ..... 1078  
||| ||||| |||||  
341 AlaGlyGluSerAlaAspGluLysMetSerValValProLeuLysTyr 357  
1079 .....GCTTCAGTCCACCAAAATTTTCTGCTACT 1106  
||||| ||||| |||||  
357 rSerHisValPheValTyrAspGlyThrValHisAsnGlnSerAspL 374  
1107 TCACHTTTGCAACTGGCGAAAATAATTGGACACATGCTCAAAATTAAAGGGA 1156  
::: ||||| |||||  
374 euProIleLeuLeuProArgMetValLeuArgValLeuLysGlyLysPhe 390  
1157 GACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGAGCTTCATTAGC 1206

```

203 ATCCCCCGGGGAAATGGCCCTTATTCGGTGTGGTACAGCACTTAATGTT 252
   ::::: ::::: ||||| ::::: ||| ::::: ::::: ::::: :::::
112 LeuProGluuproThrGlyProTyrluIleGlyValThrAsnPhelHisr 128
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
253 T.....GATCACTAAATAAGGCCA 272
   :..... ::::: ||||:
128 pValAspProAspArgGluGluValGluGlyValAsnGlyAsnArgGluL 145
   :..... ::::: ||||:
273 CCTCTTCGGCTTATATATCCATCCCAA...GATATGATCGCCCTGAC 319
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
145 euMetValArgileTrpTyrrProAlaGluLeuThrGluGlyGlyLeuTy 161
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
320 ACCCTTTGGATCCCAATAMAGAATATTTTGGGGCTCTAGCAAAATTCCT 369
   ::::: ::::: ::::: ||||| ::::: ||||| ::::: |||||
162 AlaProTyrAlaAlaPheAspProSerTyThrGluLeuValSerIysGluLe 178
   ::::: ::::: ::::: ||||| ::::: ||||| ::::: |||||
370 TGGACACACATGGCTTATGGGCACACATTTTGACGCTTACTCTTGGTTCAA 419
   | ::::: ||||| ::::: ||||| ::::: |||||
178 uproTyrTyrr.....LysAlaLeuLeuTyrrSerValI 190
   | ::::: ||||| ::::: ||||| ::::: |||||
420 TGACAACCTCGTCAAAAC.....TGGAAATCCCTCTGAGGCT...GCT 460
   ::::: ||||| ::::: ||||| ::::: |||||
190 leclnThrCluThrHisSerPheAlaAsnValProValAlaAspHisGly 206
   ::::: ||||| ::::: ||||| ::::: |||||
461 GAAAAATATCCACTTGTGTTTTCATCGTGTCTGGGGCAATTCAGGAC 510
   ||||| ||||| ::::: ||||| ::::: |||||
207 AlaProTyrrProValIleuIleuLeuSerProGlyTyrrGlyAsnSerAsnph 223
   ||||| ||||| ::::: ||||| ::::: |||||

```

hypothetical protein PA1907 [imported] - *Pseudomonas aeruginosa* (strain PAO1)



C;Species: *Pseudomonas aeruginosa*  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C;Accession: D83408  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizeguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
 A;Reference number: A82950; MUID:20437337  
 A;Accession: D83408  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-546 <STO>  
 A;Cross-references: GB:AE004091; GB:AE004616; NID:9947890; PIDN:AG05295.1; GSPDB:GN001  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA1907

alignment\_scores:  
 Quality: 162.50 Length: 437  
 Ratio: 0.781 Gaps: 18  
 Percent Similarity: 47.597 Percent Identity: 21.968

alignment\_block:

US-09-922-067-9 x D83408 ..

Align seg 1/1 to: D83408 from: 1 to: 546

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167 GACTGATGGCTGGTGCAGC.....TTTGGCCAAACTAAATCCC 207
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 ValLeuAlaLeuAlaLeuAlaLeuTyLeuProValAlaProLeu 105

208 CCGGGAATGGCCCTTATTCCTGGTGTGACAGACTTAATGTTGATC 257
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
105 AlaProSerGlyProTyrAlaValGlyValArgAspHeuLeuAsp 122

258 ACACATAAAG.....GGCACC..... 274
|||||:|||||:|||||:|||||:|||||:|||||:
122 spProSerArgProGlyLeuLeuGlyThrProAlaGlyGlnProArg 138

275 ....TCTTGGCTTATATATCCATCCCAAGATAATGATCCCTGACAC 321
|||||:|||||:|||||:|||||:|||||:|||||:
139 LeuValArgAlaTyrProAlaArg.....ProIl 150

322 CCTTTGGATCCCAATAAAGATATTTT..... 349
|||||:|||||:|||||:|||||:|||||:|||||:
150 eAlaGlyAlaAlaProArgHisTyrPheAspProGlyGluAlaArg 167

350 ....TGGGCTTAGCAATTTCTTGAACACACTGGCTTAIGGGCAAC 394
|||||:|||||:|||||:|||||:|||||:|||||:
167 hAlaArgGlyPheGlyGluLeuGlyPheProLeuLeuThrTyr 183

395 ATTTGAGGTACTCTTGGTCAATGACAACTCCTGCCAACTGGAATTC 444
|||||:|||||:|||||:|||||:|||||:|||||:
184 LeuLysHisLeuArgThrAsnSerTyrPro.....AspAl 195

445 CCTCTGAGG.....CCTGGTGAATAATCCACTTGTGTTTCTCATG 491
|||||:|||||:|||||:|||||:|||||:|||||:
195 aProLeuArgAspSerAlaArgLeuProValPheTyrSerHisG 212

492 GTCTGGGGCATTCAGGACACTTTTATCTGCTATGCGATTGACCTGGCA 541
|||||:|||||:|||||:|||||:|||||:|||||:
212 LtyrSerAlaPheAlaGlyGlyAsnTyrThrLeuMetGluLeuAla 228

542 TCATCGCTGTTTATGCTGCTAGAACACAGATAGATCGCATC 591
|||||:|||||:|||||:|||||:|||||:|||||:
229 SerHisGlyTyrAlaValTyrAlaLeuGlnHisSerGly..... 241

592 TGCAACTTACTATTTCAAGGACCAATCTGTCAGAAATAGGGCAAGT 641
|||||:|||||:|||||:|||||:|||||:|||||:
242 .....AspAlaSerProThrArgLeuProAspGlyT 252

```

```

642 CTTGGCTTACCTTAGAACCCCTGAACAGAGGAGGACACATATACGA 691
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252 hLeuLeuProMetAspProGlyLeuValGluHisLeuArgAlaAla 268

692 AATGACAGGTACGGCAAGAACAAAGAA.....TGTCCCAAGCTCT 735
|||||:|||||:|||||:|||||:|||||:|||||:
269 HisAspGlyLeuProGlnAlaMetArgGlnGlyTyrValSerAspLe 285

736 CACTCTGATCTTGAC.....ATTGATCATGCAAGC 767
|||||:|||||:|||||:|||||:|||||:|||||:
285 uAspGlnArgLeuAspGlyClnLeuHisThrAlaLeuAspLeuProAla 302

768 CAGTGAAGATGATTAAGTAAAG..... 793
|||||:|||||:|||||:|||||:|||||:|||||:
302 roAlaAsnArgAlaValAsnLeuSerAlaProValTyrLeuAlaAspArg 318

794 ...TTTGATATGGAACAACACTGAAGGACTCTATTGATAGGAAAAATAGC 840
|||||:|||||:|||||:|||||:|||||:|||||:
319 LeuPheValHisAspArgLeuGlnAlaGlyGluValProAspArgValAl 335

841 A.....GTAATTGGACATT 854
|||||:|||||:|||||:|||||:|||||:|||||:
335 aAspLeuValAlaAlaSerAspPheAlaHisThrGlyGluMetGlyMetS 352

855 CTTTGTGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTC 904
|||||:|||||:|||||:|||||:|||||:|||||:
352 erPheGlyGlySerThrGlyAlaValCysMetValAspArgArgCys 368

905 AGATGCTGATTCCTGCTGATGATGATGTTTCCACTGGGTGATCAAGT 954
|||||:|||||:|||||:|||||:|||||:|||||:
369 AlaAlaAlaValAsnLeuAspGlyGlyAspPheAspPheAla...ProPh 384

955 ATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTCC 1004
|||||:|||||:|||||:|||||:|||||:|||||:
384 eAspSerAspPheProAlaProLeuLeuMetLeuHisAlaAspLeu... 399

1005 AATATCCTGCTAATATCATATAAATGAAAAATGCTACTCCTCATATAA 1054
|||||:|||||:|||||:|||||:|||||:|||||:
400 .....GlyAsnPheTyrArgLeuPheGlyLeuGluProAlaArg 413

1055 GAAAGAAAGATG..... 1066
|||||:|||||:|||||:|||||:|||||:|||||:
414 ProArgSerPheAsnAspPheSerTyrGluArgPheGluHisAlaGlyL 430

1067 .....ATTACATCAGGGGTTTCAGTCCACAGAAAT 1097
|||||:|||||:|||||:|||||:|||||:|||||:
430 nArgGlnAspIleHisArgLeuValLeuArgAspSerAlaHisAlaGlyL 447

1098 TTGCTGACTTCACCTTTTGCACACTGGCAAAATAATGGACACATGCTCAA 1147
|||||:|||||:|||||:|||||:|||||:|||||:
447 euThrAsp.....AsnProLeuPheIleArgArgProLeuArg 459

1148 .....TTAAGGGAGACATAGATTCAATGCGAGCTATTGATCTTAGCAA 1191
|||||:|||||:|||||:|||||:|||||:|||||:
460 AspGlyLeuLeuGlySerAlaProThrGluValLeuIleGlnAlaProAs 476

1192 CAAGCTTCATTAGCTTTTACAAAGACATTTTA...GGACTTCATAAAG 1238
|||||:|||||:|||||:|||||:|||||:|||||:
476 nAlaLeuValLeuGlyPhePheAspHisTyrLeuArgGlyArgAlaAsnA 493

1239 ATTTGATCAG 1249
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493 spPheProGln 496

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seq\_name: p1r2:r36311

seq\_documentation\_block:

probable lipase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: T36311

R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, March 1999

A:Reference number: Z21604

A:Accession: T36311

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-391 <SAU>

A:Cross-references: EMBL:AL035654; PIDN:CAB38590.1; GSPDB:GN00070; SCOEDB:SCE8.12c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCE8.12c

# alignment\_scores:

Quality: 149.00 Length: 380  
Ratio: 0.801 Gaps: 12  
Percent Similarity: 48.947 Percent Identity: 20.000

# alignment\_block:

US-09-922-067-9 x T36311

Align seg 1/1 to: T36311 from: 1 to: 391

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176 GCTGCTCAGAGCTTTGGCCCAACTAAATCCCGGGGAAATGGGCTTTA 225
|||||
44 AlaAspAlaAlaTrpThrAlaSerAlaValProAlaProThrGlyAlaLe 60
226 TTGCGTTGGTTTACAGACTTAATGTTGATCACAATAAT 265
|||||
60 uProValGlyValArgThrAlaHisLeuArgAspThrSerArgArgAsp 77
266 .....
77 roTrpAsnProAspArgTyrArgGluLeuAlaLeuSerLeuTrpTyrPro 93
296 TCCACAGATAATGATCGCTTGCACACCTTTGGATCCCAATAAAGAATA 345
|||||
94 AlaLeuProSerArgAlaProArgAlaSerTyrValThrAlaArgGlu... 109
346 TTTTGGGGTCTTAGCAATTTCTTGGACACACTGGCTTATGGGC.... 391
|||||
110 .....SerAlaLeuLeuArgPheHisArgValGluGlyValP 123
392 .....AACATTTTGGGTTACTCTTTGGTTCAATGACAACTCCTGCA 433
|||||
123 roAlaAspLeuLeuAlaArgPheArgValHisAlaArgThrAlaPro... 138
434 AACTGCAATTCCTCTG...AGGCTGGTGAAATATCCACTTCTTGT 480
|||||
139 .....ProLeuProAlaProAlaArgGlyLeuProLeuValLe 152
481 TTTTCTCATGCTTGGGGCACTTTCAGACACTTTATTCTGCTATPGCA 530
|||||
152 uLeuSerProGlyPheAlaLeuProArgSerSerLeuThrGlyLeuAlaG 169
531 TTGACCTGGCATCTCATGGTTTATAGTTGCTGCTAGAACACAGAGAT 580
|||||
169 luCluLeuAlaSerArgGlyTyrAlaValAlaAlaValAspHisAlaTyr 185
581 AGATTCGCATCTGCAACTTACATTTCCTAAGGACCAATCTGCTGCAGAAAT 630
|||||
186 GluAlaProAlaIleSerHis..... 192
631 AGGGGCAAGTCTTGCTCTACCTTAGAACCTGAAACACAGGAGGAGA 680
193 .....ProAspG 195
681 CACATATACCAANTAGCAGGTTACGGCAAGCAAGAAAGATGTTCCCAA 730
|||||
195 lyArgValThrGlyCysLeuAlaCysArgArgHisProGluGlyAlaArg 211
731 GCTCTCAGTCTGATTCTTGACATTGATCATGGAAGCAGCTGAAGAATGC 780
|||||
212 ValAlaAla.....ThrArgAl 217

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```

781 ATTAGATTAAAGTTTGATATGGAACAACACTGAAGGACTCT..... 820
|||||
217 aAlaAspLeuArgPheValArgGluArgLeuArgSerProGlyAlaVal 234
821 .....ATTGATAGGGAATAATAGCAGTAATTTGGACATTCT 856
|||||
234 alGlyLeuProArgLeuAspProSerArgValAlaValAlaValGlyHisSer 250
857 TTTGTCGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTCT 906
|||||
251 MetGlyGlyAlaAlaAlaPheGluAlaLeuArgThrAspAlaGlyPheAl 267
907 ATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATCAAGTAT 956
|||||
267 aAlaAlaAlaAsnLeuAspGlyThrValHisThrGlyGly.....A 281
957 ATTTCAGAAATTCCTCAGCCCTCTTTTATCAACTCT...GAATATTTC 1003
|||||
281 rgSerProValAspArgProPheLeuLeuLeuGlyAlaGlyGluHisGly 297
1004 CAATATCCTGCTAATATCATATAAAATGAAAAATGCTACTCACCTGATAA 1053
|||||
298 ArgProGlyAlaAspProThrTrpGlnArgAlaTrpArgAspLeuSerG 314
1054 AGAAGAAGATGATTACAATCAGGGGTTCTGCTCCACCACCAATTTGCTG 1103
|||||
314 yProArgArgTrpLeuSerValArgGlyAlaGlyHisLeuSerPheThrA 331
1104 ACTTCACTTTTGCACCTGGCAAAATTAATTCGACACATGCTCAAAATAAG 1153
|||||
331 sPtyr.....AlaArgLeuLeuGluArgThr 339
1154 GGACACATAGATTCAATGCGACTATTGAT.....CT 1185
340 GlyThrAlaGlyGluGluValThrLeuGlyAlaAlaAspAlaGlyArgVa 356
1186 TAGCACAAAGCTTCATTAGCATTTCTTACAAAAGCATTTA 1225
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356 lThrArgGluLeuValValAlaPheLeuAspGluArgLeu 369

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seq\_name: pir2:P82858

# seq\_documentation\_block:

dipeptidyl-peptidase Xr0015 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: F82858  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82858  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-795 <SIM>  
A:Cross-references: GB:AE003856; GB:AE003849; NID:g9104770; PIDN:AAF82828.1; GSPDB:US-09-922-067-9  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, L.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carras-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti, A.; Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, R.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sentelli, R.V.; S.M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.  
A:Reference number: A59328  
C:Contents: annotation  
C:Genetics:





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881 ACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGATCATG 930
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397 Val.....AlaGlyAlaThrIleAsp...Tr 404
   |||      :::::      :::::      :::::      :::::      ::
931 GATGCTTTCCACTGGTGAT...GAAGTATATTCCAGAAATTCCTCAGCCCC 977
   |||      :::::      :::::      :::::      :::::      ::
404 pAspPheLeuIysSerGluCysArgIleGlyGluValProAsnThrA 421
   :::::      :::::      :::::      :::::      :::::      ::
978 TCCTTTTATCAACTCTGTAATATTCCAAATATCCTGCTAATATCATATAAA 1027
   :::::      :::::      :::::      :::::      :::::      ::
421 laLeuLeuLeuGlnCysAspAlaLeuThrLeuProArgSerAspTyrAsp 437
   :::::      :::::      :::::      :::::      :::::      ::
1028 ATGAAGAAAATGCTACTCACCTGATTAAGAAAGAAAGATGATTACAATCAG 1077
   ::      ::      ::      ::      ::      ::      ::      ::
438 Phe.....ArgAspProArgValValAlaValLe 447
   :::::      :::::      :::::      :::::      :::::      ::
1078 GGGTTCAGTCCACGAGAATTTTGCTGACTTC...ACTTTTGCACACTGCCA 1124
   :::::      |||      |||      |||      :::::      ::
447 uAlaAlaAsnProValAsnSerAlaIlePheGlyValSerGlyLeuHisL 464
   :::::      :::::      :::::      :::::      :::::      ::
1125 AAATAAATGGACACATGCTCAAAATTAAGGGAGACATAGATTCAATATGCA 1174
   ||:::      :::::      |||      ||:::      |||      ::
464 yValThrValProValLeuLeuGlyGlySerTyrAspProAlaThr 480
   :::::      :::::      :::::      :::::      :::::      ::
1175 GCTATTGATCTTAGCAACAAGCTTCA.....TTAGCATTTCTTTACA 1215
   ::      ::      |||      :::::      ||:::      ::
481 ProPheValLeuGluGlnAlaArgSerPheProArgLeuAlaSerArgAs 497
   :::::      :::::      :::::      :::::      :::::      ::
1216 AAAGCATTTAGGACTT.....CATAAAGCATTTTGCATCAGT 1250
   ||:::      |||      |||      |||      ||:::      ::
497 pLysTyrLeuThrLeuMetGluGlyGlnAlaHisValAspPheSerLysI 514
   :::::      :::::      :::::      :::::      :::::      ::
1251 GGGACTGCTTCAATTGAAGGAGATGATGAGAATCTT..... 1285
   ||:::      ||:::      :::::      ||:::      ::
514 leAspAlaAsnIleLysAsnValValGluSerValGluAlaValSerLeu 530
   :::::      :::::      :::::      :::::      :::::      ::
1286 ...ATTCCAGGAGCAAC...ATTACACAGCAACCAATCAACACATCATGTT 1329
   :::::      |||      :::::      |||      :::::      ::
531 LysLeuProAspProAsnLeuLeuHisThrTyrGlySerAlaValMetVa 547
   :::::      :::::      :::::      :::::      :::::      ::
1330 A 1330
   ::
547 I 547
seq_name: pir2:D75217
seq_documentation_block:
probable 2'-acetyl-1-alkylglycerophosph ocholine esterase PAB2176 - Pyrococcus abyssi (st
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: D75217
R:anonymous, Genoscope
submitted to the EMBL data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75217
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KAW>
A:Cross-references: GB:AJ248203; GB:AL096836; NID:g5457433; PIDN:CAB49187.1; PID:e151508
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2176

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alignment_scores:
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  Ratio: 0.889        Gaps: 13
  Percent Similarity: 42.140      Percent Identity: 22.408

alignment_block:
  US-09-923-067-9 x D75217 ..

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Align seg 1/1 to: D75217 from: 1 to: 286

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206 CCCCGGGAAATGGCCCTATTCCGTTGGTTGACAGACTTAATGTTGA 255
      ||||| ||| ::::~ ||||| ||||| |||||
29 ProArgValGlyLysTrpThrPro.....LysAspLeuGlyPheAs 43
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
256 TCACACTAATRAGGCGACCTCTTCTGGCTTATATATTCATCCCAAGATA 305
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
43 pIyrGlu.....LysValGluPheLysSerArgAspG 54
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
305 ATGATCGGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTCGGGT 355
      ||| ||| ||||| ||||| ::::~ |:::~ |:::~ |:::~
54 LylleThrLeuArgLysTrpTrpIleAspGlnGlyLys.....66
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
356 CTTAGCNAATTTCTTGGAAACACACATGGCTTATGGCAACACATTTTGAGTT 405
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
67 .....AspGluThrValIleLeu 72
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
406 ACTCTTTGGTTCAATGACAACTCTCGCAAACTGCAANTCCCTCTGAGGC 455
      ||| ||| ||| ||| ||||| ||||| |||||
72 lleuHisGly.....TyrThrAlaSerLysTrpAsn.....82
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
456 CTGGTGCAAAATAT.....CCACTGTGTGTTTTTCTCATGGCTCTGGG 499
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 .....GluValTyrMetLysProAlaIleGluIleValAlaAsnLeuGly 97
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
500 GCATTCAGGACACTTATTCGCTATTGGCAATTCACCTGGCACTCATGG 549
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
98 .....TyrAsnValLeuThrPheAspPheArgAlaHisGln 109
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
550 GTTTATAGTTGCTGTGTAAGACACAGAGATAGATCTGCATCTGCAACTT 599
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
109 Y..... 109
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
600 ACTATTTCAAGCACCAATCTGCTGCAGAAATAGGGGACAGCTCTTGGCTC 649
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
110 .....GluSerGluGlySerLysThrThrIleGlyAsp.....120
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
650 TACCTTAGAACCTGAAACAGAGGAGGAGACACATATACGAATGACGA 699
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
120 ..... 120
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
700 GSTACGGCAAGCAGCAAAAGAAATGTTCCCAAGCTCAGCTGATCTTGT 749
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
120 ..... 120
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
750 ACATTCATCATGTAAGCCAGTCAGAAATGCAATGATTTAAAGTTTCAT 799
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
121 .....LysGluIleLeuAspLeuSerGlyAla 129
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
800 ATGGAACAACTGAAGACATCTATTGATAGGGAATAATAGCAAGTAATGG 849
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
130 IleAspTrpLeuLeuSerAsnThrAsnThrLysLysIleAlaLeuIleGln 146
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
850 ACATTCCTTTGGTGAGCAACGGTATTATCAGACTCTTAGTCAGACATCAGA 899
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
146 yPheSerMetGlyAlaMetValThrIleArgAlaLeuAlaGlnAspGln 163
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
900 GATTCAGATGTGGTATTTGCCCTGGATGATGATTTTCCACTGGGTGAT 949
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
163 rgValCysGlyIleAlaAspSerProIleTyrIle.....Asp 177
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
950 GAAGTATATCCAGAAATTCCTCAGCCCTCTTTTTCATCAACTCTGAATA 999
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
178 LysThrGlyAlaArgGlyLeuLys.....TyrPheAlaAsnLeuProGln 192
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
1000 TTTCCAATATCCCTGCTAAATATCATAAA...ATGAAAAAATGCTACTCAC 1046
      ||| ||| ||||| ||||| ::::~ |:::~ |:::~ |:::~
192 upHeLeuTyrPro.....IleIleLysProPheThrLysMetPheSerG 207
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~
1047 CTGATAAGAAAGAAAGATCATTAATCAGGGGTTCAGTCCACCAG 1093
      |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~ |:::~

```

526 TGGCATTGAC...CTGGCATCTCATGGGTTTATAGTTGCTGCTGAGAAC 572

C:Accession: F71174  
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Håikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A:Reference number: A71000; MUID:98344137  
 A:Accession: F71174  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-622 <KAW>  
 A:Cross-references: GB:AP000002; NID:93236129; PID:BAA29683.1; PID:g3257000  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by Genbank  
 C:Genetics:  
 A:Gene: PH0594

alignment\_scores:  
 Quality: 110.00 Length: 290  
 Ratio: 0.932 Gaps: 14  
 Percent Similarity: 40.690 Percent Identity: 20.345

alignment\_block:  
 US-09-922-067-9 x F71174 ..

Align seg 1/1 to: F71174 from: 1 to: 622

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344 TATTTTGGGGT.....CTTAGCAAAATTTCTTGGACACA 378
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287 TyrLeuTrpAspGlyValArgGluIleAlaTys.....GlyLysHi 301
|||||.....|
379 CTGGCTTATGGGC.....AACATTTTGAGTTACTCTTTGGT 416
|||||.....|
301 strPileMetGlyPheAspAlaAspGluArgLeuIleTyrLeuLysGluT 318
|||||.....|
417 CAATGACAACTCTGCAAC.....TGGAAATTC..... 445
|||.....|
318 hrAlaThrArgProAlaGluLeuTyrLeuTrpAspGlyGluArgGln 334
|||||.....|
445 ..... 445
335 LeuThrAspTyrAsnGlyLeuIlePheLysLysLeuLysThrPheGluPr 351
|||||.....|
445 ..... 445
351 oArgHisPheArgPheLysSerIleAspLeuGluLeuAspGlyTrpTyrI 368
|||||.....|
446 .....CTCTGAGGCTGGTGAATAATATCCACTTGTCTTTTCT 487
|||||.....|
368 leuysProGluIleLysGluGlyValAlaProValIleValPheVal 384
|||||.....|
488 CATGGT.....CTTGGGCATTCAGGACACTTTATCTGCTATTGGCAT 531
|||||.....|
385 HisGlyGlyProLysGlyMetTyrGlyTyrTyrPheLysTyrGluMetGl 401
|||||.....|
532 TGACCTGGATCTCATCGGTTTATAGTTGCTGCTAGAACACACAGAGATA 581
|||||.....|
401 nleuMetAlaSerLysGlyTyrTyrIleValTyrValAsnProArgGlys 418
|||||.....|
582 GATCTGATCTGCACTTACTTATTCAGGACCAATCTGCTGCAGAAATA 631
|||||.....|
418 erAsnGly.....TyrSerGluAsp..... 424
|||||.....|
632 GGGGACAAGTCTTGGCTTACCTTAGAACCTTGAACACAGAGGAGAC 681
|||||.....|
425 .....PheAlaLeuArgValLeu.....GluArgTh 433
|||||.....|
582 ACATATACGAATGACGAGGTAGCGCAAGAGCAAAAGAAATCTCCCAAG 731
|||||.....|
433 rGlyLeuGluAspPheGln..... 439
|||||.....|
732 CTCTCACTCTGATTCTTGATGATGATGAAAGCCAGTGAAGAAATGCA 781
|||||.....|

```

```

440 .....AspileLeuAsnGly 444
782 TTAGATTAAAGTTTGATATGGACAACTGAAGGACTCTATTGATAGGGA 831
|||||.....|
445 Iledlu.....GluPheLeuArgLeuGluProGlnAlaAspArgGl 458
|||||.....|
832 AAAAATAGCAGTAATTCGACATCTTTTGGTGGACGACGCGTTATTGCA 881
|||||.....|
458 uArgGlyIleThrGlyIleSerTyrGlyTyrMetThrAsnTrpA 475
|||||.....|
882 CTCATTAGTAGAGATGACAGATTTCAGATGCTGGTATTGCC..... 919
|||||.....|
475 lateuThrGlnSerAspLeuPheLysAlaGlyIleSerGluAsnGlyIle 491
|||||.....|
920 .....CTGGATGCATGGATGTTT..... 937
|||||.....|
492 SerTyrTrpLeuThrSerTyrAlaPheSerAspileGlyLeuTrpPheAs 508
|||||.....|
938 .....CCACTGGGTGATGAAGTATATATTCAGAA 965
|||||.....|
508 pLysGluValIleGlyAspAsnProLeuGluAsnGluAsnTyrArgLysL 525
|||||.....|
966 TTCCTCAGCCCTCTCTTTT 985
|||.....|
525 eu...SerProLeuPheTyr 530
|||.....|
seq_name: pir2:T36421
seq_documentation_block:
hypothetical protein SCF34.22 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36421
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21606
A:Accession: T36421
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-326 <SAU>
A:Cross-references: EMBL:AL109974; PIDN:CAB53333.1; GSPDB:GN00070; SCOEDB:SCF34.22
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCF34.22

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alignment\_scores:  
 Quality: 108.50 Length: 217  
 Ratio: 1.119 Gaps: 9  
 Percent Similarity: 44.700 Percent Identity: 23.041

alignment\_block:

US-09-922-067-9 x T36421 ..

Align seg 1/1 to: T36421 from: 1 to: 326

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458 GGTGAAAAATATCCACTTGTGTTTTCATGCTGTGGGCATTCAG 507
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44 GlyThrGlyLeuProValIleLeuLeuSerHisGlyGlnGlyTyrSerAs 60
|||||.....|
508 GACACTT.....TATTGCTATTGGCATTCACCTGGCAT 542
|||||.....|
60 nHisLeuSerSerLeuAspGlyTyrAlaProLeuAlaThrTyrTrpAla 77
|||||.....|
543 CTCATGGGTTTATAGTTGCTGCTGTAACACACAGATAGATCTGCTATCT 592
|||||.....|
77 laHisGlyPheValIleGlnProThrHis..... 87
|||||.....|
593 GCAACTTACTATTTCAGAGCACTCTGCTGCAGAAATAGGGGACAAGTC 642
|||||.....|
87 ..... 87
643 TTGGCTCTACCTTAGAACCTTGAACAGAGGAGGACACATATACGAA 692
|||||.....|

```

```

88      ...LeuSerSerArgThrLeuAlaLeuAspProGlyThrProGlyAlaP 103
      ||| ||||| ||| :||
693  ATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTG 742
      ||||| ||||| ||||| ||||| ||||| |||||
103  roLeuPheTrpArgSerArgAlaGluAspMetThrArgValLeu..... 117
      743  ATTCTTGACATTGATCATGGAAAGCCAGCTGAAGATGCATTAGAT...TT 789
      118      :||| ||||| ||||| ||||| ||||| ||||| |||||
      790  AAGTTTGATATGGACAACTGAAGACTCTATTGATAGGAAAAAATAG 839
      123  uGluuysAlaValProGluLeuSerGlyArgLeuAspArgSerArgValA 140
      840  CAGTAATTGGACATCTTTGTGTGGAGCAACGGTTATTTCAGACCTCTTAGT 889
      140  laValaIaGlyHisSerMetGlyGlyHisThrAlaSerLeuLeuLeuGly 156
      890      :||| ||||| ||||| ||||| ||||| ||||| |||||
      157  AlaArgLeuThrAspProAspAspGlyThrGluValAspLeuThrGluPr 173
      898  GAGATTCAGATGTGGTATGTGCCCTGGATGCATGATGATTTCCA..... 940
      173  oArgileGlyAlaGlyValLeuLeuAlaIa.....ProGlyArgG 187
      941      :||| ||||| ||||| ||||| ||||| ||||| |||||
      187  LyGlyAspAlaLeuSerGluSerAlaIaGluSerMetPro..... 200
      980  TTTTTCACACTCTGAATATTTCCAATAT.....CCTCTAATATCAT 1023
      201  PhePheLeuSerThrAspPheSerArgMetThrThrProAlaLeuValVa 217
1024  A 1024
      217  I 217

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OM of: US-09-922-067-9 to: SwissProt\_39:\* out\_format : pfs  
 Date: Mar 9, 2002 12:29 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
 -MODE=framer-n4p.model -DEV=xlp  
 -Q/cgn2\_1/USPTO\_spoil/US09922067/runat\_07032002\_140446\_9437/app\_query.fasta\_1.1439  
 -DB=SwissProt\_39 -QFMT=fastan -SUFFIX=rs -GAPOP=12.000  
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000  
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
 -DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500  
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62  
 -TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
 -NORM=ext -MINLEN=0 -MAXLEN=200000000  
 -USER=US09922067\_cgn2\_1\_35 -NCPU=6 -ICPU=3 -LONGLOG -NO\_XLPY  
 -WAIT -THREADS=1

Search information block:  
 Query: US-09-922-067-9  
 Query length: 1361  
 Database: SwissProt\_39:\*  
 Database sequences: 100059  
 Database length: 36664827  
 Search time (sec): 78.140000

Sequence	Strid	Orig	ZScore	EScore	Len
SwissProt_39:PAPA_HUMAN	2354.00	3570.52	7.5e-192	441	013093
SwissProt_39:PAPA_BOVIN	1964.50	2977.71	7.8e-159	444	Q28017
SwissProt_39:PAPA_CANFA	1935.50	2933.57	2.2e-156	444	Q28262
SwissProt_39:PAPA_CAYPO	1572.50	2381.30	1.3e-125	436	P70683
SwissProt_39:PAPA_MOUSE	1515.50	2294.48	9.0e-121	440	Q50963
SwissProt_39:PAPA_CHICK	1131.50	1710.45	3.2e-88	422	Q30678
SwissProt_39:PAF2_HUMAN	797.00	1202.03	7.1e-60	392	Q39487
SwissProt_39:PAF2_BOVIN	747.00	1125.94	1.2e-55	392	P79106
SwissProt_39:PAPA_CAEEL	493.50	738.50	3.9e-34	476	Q22943
SwissProt_39:DAP1_YEAST	103.50	139.27	0.4710	931	P33894
SwissProt_39:STPC_CANAL	100.50	138.81	0.8091	575	P78600
SwissProt_39:CLPP_CHLEU	99.50	132.49	1.04	1010	P42379
SwissProt_39:APY_AEDAE	99.00	136.72	1.08	562	P50635
SwissProt_39:SYR_HELJP	96.00	132.48	1.94	541	Q92mb9
SwissProt_39:CNRB_HUMAN	95.50	127.83	2.23	854	P35913
SwissProt_39:ESTP_DROME	95.00	130.91	2.35	544	P18167
SwissProt_39:RS1_CHLVR	95.00	130.53	2.36	569	Q84100
SwissProt_39:JBN1_YEAST	95.00	129.85	2.38	616	P36035
SwissProt_39:LECF_ALEAU	94.00	134.13	2.72	312	P38891
SwissProt_39:PRXV_ASCNO	94.00	129.19	2.87	557	P81701
SwissProt_39:RS1_CHLMO	94.00	128.99	2.87	570	P38016
SwissProt_39:OPSD_CAMMA	93.00	132.94	3.29	300	Q38315
SwissProt_39:SNZ1_YEAST	92.50	132.26	3.63	297	Q03148
SwissProt_39:LIP_PSEAE	92.50	131.87	3.64	311	P26876
SwissProt_39:LIP_PSEEP	92.50	131.87	3.64	311	P26877
SwissProt_39:SVL_SNY3	92.00	121.26	4.47	988	P73505
SwissProt_39:TRNU_HELJP	91.50	129.10	4.49	360	Q35893
SwissProt_39:DP4_RAT	91.50	122.66	4.81	767	P14740
SwissProt_39:MUS2_SNY3	91.50	122.07	4.84	822	P73625
SwissProt_39:TRPE_HELJP	90.50	124.78	5.62	500	Q35869
SwissProt_39:ESTC_DROPS	90.50	123.29	6.25	545	P25725
SwissProt_39:DHE4_HUMAN	90.00	123.09	6.26	558	P49448
SwissProt_39:LVTB_STRPN	90.00	121.68	6.36	658	Q924p7
SwissProt_39:TRPE_HELJD	89.50	123.26	6.84	500	Q824j5
SwissProt_39:C57A_PIG	89.50	123.24	6.84	501	Q46491
SwissProt_39:NOS_RHOP	89.50	115.99	7.40	1174	Q26240
SwissProt_39:ESTA_DROPS	89.00	121.78	7.60	544	P25727
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SwissProt_39:MX1A_RAT	89.00	115.51	8.13	1136	Q05096
SwissProt_39:OPSD_CAMLU	88.50	126.06	7.93	301	Q16017

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 AC Q13093; Q15692;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 DT 20-AUG-2001 (Rel. 40; Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (LDL-ASSOCIATED  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7 OR PAFAH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.  
 RC TISSUE=Myeloid;  
 RX Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,  
 RA Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,  
 RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;  
 RT "Anti-inflammatory properties of a platelet-activating factor  
 acetylhydrolase.";  
 RL Nature 374:549-553(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=96197208; PubMed=8624782;  
 RA Tew D.G., Southern C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,  
 RA Moores K., Glover I.S., Macphie C.H.;  
 RT "Purification, properties, sequencing, and cloning of a lipoprotein-  
 associated, serine-dependent phospholipase involved in the oxidative  
 modification of low-density lipoproteins.";  
 RL Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).  
 RN [3]  
 RP MUTAGENESIS.  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
 RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
 RA Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 RN [4]  
 RP VARIANT PHE-279.  
 RX MEDLINE=96259525; PubMed=8675689;  
 RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,  
 RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,  
 RA McIntyre T.M., Gray P.W., Prescott S.M.;  
 RT "Platelet-activating factor acetylhydrolase deficiency. A missense  
 mutation near the active site of an anti-inflammatory  
 phospholipase.";  
 RL J. Clin. Invest. 97:2784-2791(1996).  
 RN [5]  
 RP VARIANT PHE-279.  
 RX MEDLINE=98430412; PubMed=9759612;  
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,  
 RA Yoshimizu N., Fukushi K., Satoh K.;  
 RT "A mutation in plasma platelet-activating factor acetylhydrolase  
 (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not  
 for hypertension.";  
 RL Thromb. Haemost. 80:372-375(1998).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY

CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS  
 CC PRESENT IN 2% OF JAPANESE. IT COULD HAVE A SIGNIFICANT  
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY  
 CC RESPONSES.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC -----  
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DR EMBL; U20157; AAC50126.1; -;  
 DR MIM; U24577; AAB04170.1; -;  
 DR MIM; 601690; -;  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 441  
 FT PLATELET-ACTIVATING FACTOR  
 FT ACETYLDIHYDROLASE.  
 FT CHARGE RELAY SYSTEM.  
 FT CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 273 273  
 FT ACT\_SITE 296 296  
 FT ACT\_SITE 351 351  
 FT CARBOHYD 423 423  
 FT CARBOHYD 433 433  
 FT VARIANT 279 279  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT V -> F (IN PLA2G7 DEFICIENCY; INACTIVE  
 FT PROTEIN).  
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 FT S-2A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 FT S-2A: LOSS OF ACTIVITY.  
 FT D-2A: ALMOST NO ACTIVITY.  
 FT D-2A: DIMINISHED ACTIVITY.  
 FT D-2A: LOSS OF ACTIVITY.  
 FT D-2A: LOSS OF ACTIVITY.  
 FT D-2A: NO CHANGE IN ACTIVITY.  
 FT D-2A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 FT H-2A: LOSS OF ACTIVITY.  
 FT V -> A (IN REF. 2)  
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## alignment\_scores:

Quality: 2354.00 Length: 441  
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## alignment\_block:

US-09-922-067-9 x PAFA\_HUMAN

Align seg 1/1 to: PAFA\_HUMAN from: 1 to: 441

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 88 TGTGGTTTATCTTTTTCAGCTGCATACATAAAATCTCTGTCGCCATATGA 137  
 17 aValValIyrProPheAspIrpGlnIyrIleAsnProValAlaHisMetL 34  
 138 AATCATACGATGGGTCAACAAAATACAAAGTACTGATGGCTGGCTGCAAGC 187

34 ySerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50  
 188 TTTTGCCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGGTGGTGG 237  
 51 PheGlyGlnIyrLysIleProArgGlyAsnGlyProIyrSerValGlyCy 67  
 238 TACAGACTTAATGTTGATCATCACTAATAAGGACACCTTCTTGGCTTAT 287  
 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84  
 288 ATTATCCATCCCAAGATAATCATCGCTTGACACCCCTTGGATCCCAAT 337  
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 388 GGCAACAATTTTGGAGTACTCTTCTTGGTTCATGACACACTCCGCAACT 437  
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 167 uAlaSerHisGlyPheIleValAlaValGluHisArgAspArgSera 184  
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seq\_documentation\_block:  
 ID PAFA\_BOVIN STANDARD; PRT; 444 AA.  
 AC Q28017;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7.  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
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 RC TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 phospholipase A2 with a catalytic triad."  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC -----  
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 CC -----  
 CC EMBL; U34247; AAC48483.1; -

DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
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 FT CHAIN 22 444  
 FT ACT\_SITE 274 274  
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1285 TATTCAGGAGCAACATTAACACCAACCAACCAACCAACCAACCAACCAACCAAC 1334  
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417 uIleProGlyThrAsnIleAsnThrThrAsnHisGlnAlaIleLeuGlnA 434  
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1335 ACTCTTCAGGAATAGAAATACAAT 1360  
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434 snSerThrGlyIleGluArgProAsn 442  
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seq\_name: SwissProt\_39:PAFA\_CANFA

seq\_documentation\_block:

ID PAFA\_CANFA STANDARD; PRT; 444 AA.

AC Q28262;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)

DE (PAF ACETYLHYDROLASE) (PAF 2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE

DE PHOSPHOLIPASE A2) (LDL-PLA-2) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE

ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
PLA2G7.  
Canis familiaris (Dog).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
NCBI\_TaxID=9615;  
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RN  
RP  
SEQUENCE FROM N.A.  
RC  
TISSUE-Spleen;  
RX  
MEDLINE=96029630; PubMed=7592717;  
RA  
TJocleik L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
RA  
McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
RT  
"Plasma platelet-activating factor acetylhydrolase is a secreted  
phospholipase A2 with a catalytic triad";  
RL  
J. Biol. Chem. 270:25481-25487(1995).  
CC  
-1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC  
INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC  
RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC  
PHOSPHOLIPIDS.  
CC  
-1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC  
H(2O) -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC  
-1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC  
-1- TISSUE SPECIFICITY: PLASMA.  
CC  
-1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC  
HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
CC  
-----  
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send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
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DR  
EMBL: U34246; AAC48484.1; -.  
DR  
InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
DR  
InterPro: IPR000734; Lipase.  
DR  
PROSITE: PS00120; LIPASE\_SER; 1.  
KW  
Hydrolase; Lipid degradation; Glycoprotein; Signal.  
FT  
SIGNAL 1 21  
FT  
CHAIN 22 444  
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ACT\_SITE 274 274  
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ACT\_SITE 297 297  
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CARBOHYD 60 60  
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SEQUENCE 444 AA; 50136 MW; 814EF0AE38B074AC CRC64;

alignment\_scores:

Quality: 1935.50

Ratio: 4.686

Percent Similarity: 93.439

Percent Identity: 80.769

alignment\_block:

US-09-922-067-9 x PAFA\_CANFA

Align seg 1/1 to: PAFA\_CANFA from: 1 to: 444

38 ATGGTCCCAACCAATTCATGCTGCTTTTCTGCTCTGCGGCTGCTGCGC 87

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1 MetLeuProProlLysLeuHisAlaLeuPheCysLeuCysSerCysLeuTh 17

88 TGTGGTTTATCCTTTTACTGGCAATACATAATCTGTTGCCCATATCA 137

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17 rLeuValHisProIleAsnPrpGlnAspLeuAsnProValAlaHisIleA 34

138 AATCATCAGCATGGGTCAACAAATAACAAGTACTGATGCTGCTGCAAC 187

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34 rgSerAlaTrpAlaAsnLysIleGlnAlaLeuMetAlaAlaSer 50

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189 ::::::::::::::::::::::::::::::::::::::::::::::
51 IleArgGlnSerArgIleProLysGlyAsnGlySerTyrSerValGlyC 67
238 TACAGACTTAATGTTGTATCAGCTAATAAGGGCACCTCTCTCGGTTAT 287
239 ::::::::::::::::::::::::::::::::::::::::::::::
67 sthrAspLeuMetPheAspTyrThrAsnLysGlyThrPheLeuArgLeu 84
288 ATTATCCATCCCAAGATAATCATGCCCTTGACACCCCTTGGATCCCAAT 337
289 ::::::::::::::::::::::::::::::::::::::::::::::
84 yTyrProSerGlnGluAspAspPheSerAspThrLeuThrPheProAsn 100
338 AAAGAAATATTTTGGGGCTTATAGCAAAATTTCTTGGAAACACACTGGT 387
339 ::::::::::::::::::::::::::::::::::::::::::::::
101 LysGluTyrPhePheGlyLeuSerLysTyrLeuGlyThrProThrLeuMe 117
388 GGCGACATTTTGGAGTTACTCTTGGTTCAATGACAACTCCCTGCAACT 437
389 ::::::::::::::::::::::::::::::::::::::::::::::
117 tGlyLysIleLeuSerPhePheGlySerValThrProAlaAsnT 134
438 GGAATTCCTCTGAGGCTGGTGAATAATCCACCTGTGTGTTTCT 487
439 ::::::::::::::::::::::::::::::::::::::::::::::
134 rPAsnSerProLeuArgThrGlyGluLysTyrProLeuIleValPheSer 150
488 CATGCTCTGGGCAATTCAGGACACTTATTCCTGCTATTGSCATTGACCT 537
489 ::::::::::::::::::::::::::::::::::::::::::::::
151 HisGlyLeuGlyAlaPheArgThrIleTyrSerAlaIleGlyIleAspLe 167
538 GCATCTCATGGCTTTATAGTTGCTGCTGTAGAACAGAGATAGATCTG 587
539 ::::::::::::::::::::::::::::::::::::::::::::::
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588 CATCTCAACTTACTATTTCAGGACCAATCTGCTGAGAAATAGGGAC 637
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184 lAsrAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsn 200
638 AGTCTTGCTCTTACTTTAGAACCTGAACAA...GAGGAGGAGACACA 684
639 ::::::::::::::::::::::::::::::::::::::::::::::
201 LysSerTrpSerTyrLeuGlnGluLysLysProGlyAspGluGluIleH 217
685 TATACGAATAGCAGGTACGCAAGCAAGCAAGAAAGATGTTCCCAAGCTC 734
686 ::::::::::::::::::::::::::::::::::::::::::::::
217 sValArgAsnGluGlnValGlnLysArgAlaLysGlyCysSerGlnAla 234
735 TCAGTCTGATTTGACATTGATCATGATGAAAGCCAGTCAGACATGATTA 784
736 ::::::::::::::::::::::::::::::::::::::::::::::
234 euAsnLeuIleLeuAspIleAspHisGlyArgProIleLysAsnValLeu 250
785 GATTATAAGTTTGATGATGAACAACACTGAAGACTCTATTGATAGGAA 834
786 ::::::::::::::::::::::::::::::::::::::::::::::
251 AspLeuGluPheAspValGluGlnLysAspSerIleAspArgAspLy 267
835 AATAGCAGTAATGGACATCTTTTGGTGGAGCACGGTTATTTCAGACTC 884
836 ::::::::::::::::::::::::::::::::::::::::::::::
267 sIleAlaValIleGlyHisSerPheGlyGlyAlaThrValLeuGlnAla 284
885 TTAGTGAAGATCAGACATTACATGCTGATGTCCTGATGATGATGATG 934
284 euSerGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMet 300
935 TTTCCACTGGGTGATGAAGTATATTCACAAATTCCTCAGCCCTCTTTT 984
936 ::::::::::::::::::::::::::::::::::::::::::::::
301 LeuProLeuAspAlaIleTyrSerArgIleProGlnProLeuPhePh 317
985 TATCAACTCTGAATATTTCCATATTCCTGCTAATATCAATAAATGAAA 1034
986 ::::::::::::::::::::::::::::::::::::::::::::::
317 eIleAsnSerGluArgPheGlnPheProGluAsnIleLysMetLysL 334
1035 AATGCTACTACCTGATATAAGAAAGAAAGATGATTACATCAGGGGTTC 1084
1036 ::::::::::::::::::::::::::::::::::::::::::::::
334 yScyTyrSerProAspLysGluArgLysMetIleThrIleArgGlySer 350

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1085 GTCCACCAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATATTTGG 1134
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1135 ACATCTCTCAAAATTAAGGGAGACATAGATTCAATGCGACTTATGATC 1184
1136 ::::::::::::::::::::::::::::::::::::::::::::::
367 yTyrIlePheThrLeuLysGlyAspIleAspSerAsnValAlaIleAsp 384
1185 TTAGCAACAAAGCTTCATTAGCATCTTACAAAGCATTTAGGACTTCAT 1234
1186 ::::::::::::::::::::::::::::::::::::::::::::::
384 euCysAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuArg 400
1235 AAAGATTTTTCATCAGTGGGACTGCTTCATTGATGAGGAGATGATGAGATCT 1284
401 LysAspPheAspGlnTrpAspSerLeuIleGluGlyLysAspGluAsnLe 417
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seq_name: SwissProt_39:PAFA_CAVPO
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ID PAFA_CAVPO STANDARD: PRT: 436 AA.
AC P70683;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN PLA2G7 OR PAFAH.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=Liver;
RX MEDLINE=97103479; PubMed=8947850;
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
RA Yokoyama K., Setaka M., Nojima S.;
RT "Cloning, expression and characterization of plasma
RT platelet-activating factor-acetylhydrolase from guinea pig.";
RL J. Biochem. 120:838-844(1996).
CC -I- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -I- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D67037; BAA11054.1;
CC InterPro: IPR000739; Est_lip_thioest_actsite.
CC InterPro: IPR000739; Lipase.

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201 ArgSerTrpIleTyrTyrLysVal.....GlyAsnLeuGluThrGluCl 215
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688 ACGAAATGAGCAGGTACGGCAAGAGCAAAAGAATGTTCCCAAGCTCTCA 737
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215 uArgLysArgGlnLeuArgGlnArgGlyGluGluCysSerGlnAlaLeuS 232
    ::::::::::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
738 GTCGTATCTTTGACATTCATCATGAAAGCCAGTCAAGCAATGCATTAGAT 787
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232 erTrpLeuLeuSerIleAspGluGlyGluProValLysAsnValLeuAsp 248
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[illegible]

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938 CCACCTGGTGATGAAGTATATTTCCAGAAATCTCTCAGCCCTCTTTTAT 987
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988 CAACCTCGAATATTTCCAAATATCTCGTAAATATCAATAAATAAGAAAAAT 1037
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1038 GCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTCAGTC 1087
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1288 TCCAGGGGACCAATTAAACACAAACCAATCAACATCATCTGTTACAGAAAT 1337
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1338 CTTTCAGGAATAGAGAAATCAAT 1360
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427 erThrGlyThrGluGlnArgAsn 434
Name: Swissprot_39:PAPA_MOUSE
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Q60963;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
(PAELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.
(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LIDL-ASSOCIATED
PHOSPHOLIPASE A2) (LIDL-PLA(2)) (2-ACETYL-L-ALKYLGLYCEROPHOS
ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
PLA2G7 OR PAFAH.
Mus musculus (Mouse)

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seq\_documentation block:

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seq_documentation_block:
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AC	060963:			

AC Q60963;  
DT 01-NOV-1997 (Re) 35 (Created)

DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last Generated)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation updates)

DE  
DE  
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE P

DE  
SE  
SE  
DE

(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE)  
PARIETAL ACTIVATING FACTOR ACETYLHYDROLASE

DE (PAF ACETYLHYDROLASE) (PAF 2-ACETHYLHYDROLASE)  
DE PHOSPHOLIPASE A2 (LDL-PLA(2)) (2-ACETYL-1-AL

DE PHOSPHOLIPASE A2 (LPL-PLA2) (2-ACETYL-1-AL-  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOL-  
DE

GN PI2G7 OR PAFAH  
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOL

GN PLA2G7 OR PAFAH.  
OS Mus musculus (Mouso)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
 RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
 RA Gray P.W.;  
 RT \*Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.\*;  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 CC -----  
 DR EMBL: U34277; AAC52274.1; ..  
 DR MGD: MGI:1351327; Pla2g7.  
 DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro: IPR000734; Lipase.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 440 PLATELET-ACTIVATING FACTOR  
 FT FT ACETYLHYDROLASE.  
 FT ACT\_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

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Quality: 1515.50 Length: 442  
 Ratio: 4.031 Gaps: 2  
 Percent Similarity: 85.068 Percent Identity: 66.516

## alignment\_block:

US-09-922-067-9 x PAFA\_MOUSE ..

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 1 MetValProLeuLysLeuGlnAlaLeuPheCysLeuPheCysLeuPhe 17  
 88 TGTGGTTTATCTTTTTCAGCTGGCAATACATAAACTCTGCTGCCCATATGA 137  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 17 oTPValHisProPheHisTrpGluAspThrSerPhe... AspPheA 33  
 138 AATCATCATGCTGGGTGCAACAATAACAAAGTACTGATGCTGCTGGCAAGC 187  
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188 TTTGGCCAACTAAATCCCGGGGAATGGCCCTTATTCGCTGGTTG 237  
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 50 SerGlyHisSerLysIleProLysGlyAsnGlySerTyrProValGlyCys 66  
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 238 TACAGACTTAATGTTTGATCACACATAATAAGGCACCTCTCTGGCTTTAT 287  
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 66 sThraspLeuMetPheGlyTyrGlyAsnGluSerValPheValArgLeu 83  
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 83 yrTyrProAlaGlnAspGlnGlyArgLeuAspThrValTrpIleProAsn 99  
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 338 AAAGAATATTTTGGGGTCTTACCAATTTCTTGGAAACACACTGCTTTAT 387  
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 388 GGCAACACTTTTTCAGGTCTACTCTTGGTTCAATGACACTCTCTCAAACT 437  
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 116 lGlyAsnIleLeuHisLeuLeuTyrGlySerLeuThrProAlaSer 133  
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 438 GGAATCCCTCTGAGGCTGGTGAATAATATCCACTTCTGCTTTTCTCT 487  
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 133 rPasnSerProLeuArgThrGlyGluLysTyrProLeuIleValPheSer 149  
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 488 CATGGCTCTGGGCATTTCAGGACACTTTTCTGCTATTGGCAATGACT 537  
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 150 HisGlyLeuGlyAlaPheArgThrIleTyrSerAlaIleGlyIleGlyLe 166  
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 538 GGCACTCATGTTGGTATTACTTCTGCTCTAGAACACACAGATAGATCTG 587  
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 166 uAlaSerAsnGlyPheIleValAlaThrValGluHisArgAspArgSera 183  
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 588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATATGGGAC 637  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 183 laSerAlaThrTyrPhePheGluAspGlnValAlaAlaLysValGluAsn 199  
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 638 AAGCTTGGCTCTACCTTAGAACCCGAAACACAGAGAGGAGACACATAT 687  
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 200 ArgSerTrpLeuTyrLeuArgLysValLysGlnGluLysSerGluSerVa 216  
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 688 ACAGAAATGACAGGTAGCGCAAGACAAAGAAATGTTCCCAAGCTCTCA 737  
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 216 lArgLysGluGlnValGlnGlnArgAlaIleGluCysSerArgAlaLeu 233  
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 738 GTCTGATCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787  
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 233 erAlaIleLeuAspIleGluHisGlyAspProLysGluAsnValLeuGly 249  
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 788 TTAAGTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 837  
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 250 SerAlaPheAspMetLysGlnLeuLysAspAlaIleAspGluThrLysI 266  
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 838 AGCAGTAATGGACATCTTCTGCTGGAGCAACGGTTATTTCAGACTCTTA 887  
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 266 eAlaLeuMetGlyHisSerPheGlyGlyAlaThrValLeuGlnAlaLeu 283  
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 888 GTGAAGATCAGAGATTCAGATGTTGTTATTCCTGCTGATGATGATGAT 937  
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 283 erGluAspGlnArgPheArgCysGlyValAlaLeuAspProTrpMetTyr 299  
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 938 CCAGCTGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTAT 987  
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 300 ProValAsnGluGluLeuTyrSerArgThrLeuGlnProLeuLeuPhe 316  
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 988 CAATCTCTGAATTTTCCAAATATCTGCTAATATCATATAAATAAATAA 1037  
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 316 eAsnSerAlaLysPheGlnThrProLysAspIleAlaLysMetLysLysP 333  
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 1038 GCTACTCACCTGATAAAGAAGAAGAAGAT GATTACAAATCAGGGGTTCAGT 1086  
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 333 heTyrGlnProAspLysGluArgLysAsnAspTyrAsnGlnGlyLeuArg 349  
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 1087 CCACCAAGATTTTCTGCTGACTTCATCTTTTGGCACTGGCAAAATAATTGGAC 1136



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350 .HISGlnAsnPheAspAspPheThrPheValThrGlyLysIleIleGlyA 366
1137 ACATGCTCAAAATTAAGGAGACATAGATTCAATGCAGCTATTGATCTT 1186
366 snLysLeuThrLysGlyGluIleAspSerArgValAlaIleAspLeu 382
1187 AGCAACAACCTTCATTAGCATCTTACAAAACATTTAGGACTTCATAA 1236
383 ThrAsnLysAlaSerMetAlaPheLeuGlnLysHisLeuGlyLeuGln 399
1237 AGATTTTGATCAGTGGCAGCTGCTGATTGAAGGAGATGATGAGAATCTTA 1286
399 sAspPheAspGlnTrpAspProLeuValGluGlyAspAspGluAsnLeu 416
1287 TTCAGGAGCACCATTTACACAAACCAATCAACACATCATGTTACAGAAC 1336
416 leProGlySerProPheAspAlaValThrGlnAlaProAlaGlnGlnHis 432
1337 TCTTCAGGAATAGAGAAATACAAT 1360
433 SerProGlySerGlnThrGlnAsn 440
seq_name: SwissProt_39:PAFA_CHICK

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seq_documentation_block:
ID PAFA_CHICK STANDARD; PRT; 422 AA.
AC 090678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN PLAZG7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RX MEDLINE-96029630; PubMed-7592717;
RA Tjoelker L.W., Eberhardt C., Under J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U34278; AAC59717.1;
CC InterPro: IPR000379; Est_lip_thioest_actsite.
CC InterPro: IPR000734; Lipase.

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DR PROSITE: PS00120; LIPASE_SER; 1
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 422 PLATELET-ACTIVATING FACTOR
FT ACETYLHYDROLASE.
FT ACT_SITE 266 266 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 289 289 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 422 AA; 47046 MW; 15A3C794376E9141 CRC64;

alignment_scores:
Quality: 1131.50 Length: 416
Ratio: 3.482 Gaps: 7
Percent Similarity: 78.125 Percent Identity: 55.288
alignment_block:
US-09-922-067-9 x PAFA_CHICK
Align seg 1/1 to: PAFA_CHICK from: 1 to: 422

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2 AlaSerLeuTrpValArgAlaArgValPheMetLysSerArgAla 18
176 .....GCTGCTGCAAGCTTTGGCCAA..... 196
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18 rGlyPheSerAlaLysAlaAlaThrGluMetGlySerGlyAlaGlu 35
197 .....ACTAAATCCCGGGGAAATGGGCTTATTCCGTTGCTGTGACA 241
:|||||:|||||:
35 ySGlyTyArgIleProAlaGlyGlySerProHisAlaValGlyCysThr 51
242 GACTTAATGTTGATCACAATAAAGGCACCTTCTGCTGTTATATTA 291
|||||:|||||:
52 AspLeuMetThrGlyAspAlaAlaGluGlySerPheLeuArgLeuTyr 68
292 TCCATCC...CAAGATAATGATCCCTTGACACCCCTTGATCCCCAAATA 338
1 :|||||:|||||:
68 rLeuSerCysAspAspThrAspThrGluGluThrProTrpIleProAsp 85
339 ACAAATATTTTGGGTCTTAGCAAAATTTCTTGGAAACACACAGCTTATG 388
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85 ySGluTyTrGlnGlyLeuSerAspPheLeuAsnValTyArgAlaLeu 101
389 GGC...AACATTTTGAGTTTACTCTTTGCTTCAATGACAACTCCTGCAA 435
||| :|||||:
102 GlyGluArgLeuPheGlnTyTrValGlySerValThrCysProAla 118
436 CTGCAATTCCTCTGAGCGCTGGGGAATAATCCACTGTGTTT 485
:|||||:|||||:
118 sSerAsnAlaAlaPheLysProGlyGluLysTyTrProLeuLeuValPhe 135
486 CTCATGCTCTGGGCGCATTCAGGACACTTTATCTGCTATTGGCATTTGAC 535
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135 eHisGlyLeuGlyAlaPheArgThrIleTySerAlaIleCysIleGlu 151
536 CTGGCATCTCATGGGTTTATAGTTCTGCTGTAGAACACAGAGATAGATC 585
:|||||:|||||:
152 MetAlaSerGlnGlyPheLeuAlaAlaValGluHisArgAspGlu 168
586 TGCATCTGCAACTTACTATTTCAGGAGCAATCTGCTGCAGAAATAGGG. 634
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168 rAlaSerAlaThrTyPheCysLysLysLysAlaAspSerGluProGlu 185
635 .....GACAAGTCTTGCTCTACCTTAGAACCTG 664
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185 luAspGlnThrSerGlyValGluLysGluTrpIleTyTrArgLysLeu 201
665 AAACAA...GAGGAGGAGACACATATACGAATGAGCAGGTACGCAAG 711
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202 ArgAlaGlyGluGluArgCysLeuArgHisLysGlnValGlnGln 218

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712 AGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCCTTGACATTCATCATG 761  
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218 gAlaGlnGluCysIleLeuAlaLeuAsnLeuIleLeuLysIleSerSerg 235  
762 GAAAGCCAGTGAAGATGATTCATAGATTTAAAGTTTGATATGGAACAACATG 811  
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235 LyGluGluValMetAsnValLeuAsnSerAspPheAspTrpAsnHisLeu 251  
812 AAGGACTCTATTCATAGAGGGAAGAAATACAGATTAATTCGACATCTTTTGG 861  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
252 LysAspSerValAspThrSerArgIleAlaValMetGlyHisSerPheGlu 268  
862 TGGAGCAAGCGGTATTTCAGACATCTTAGTGAAGATCAGAGATTCAGATGTG 911  
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268 yGlyAlaThrValIleGluSerLeuSerLysGluIleArgPheArgCysG 285  
912 GTATTCCCTGGATCGATGGATGTTTCCACTGGGTGATCAAGTATAT... 958  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
285 yIleAlaLeuAspAlaIlePheMetLeuProValGlyAspSerPheTrpGln 301  
959 TCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGATATTTTCCAATA 1008  
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302 SerSerValGlnGlnProLeuPheIleAsnSerGluLysPheGlnTr 318  
1009 TCCTGCTAATATCATAAATGAATAATGCTACTCCTCATGAAGAAA 1058  
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318 pAlaAlaAsnIleLeuLysMetLysLeuSerSerAsnAspThrAsnL 335  
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335 yIleMetIleThrIleLysGlySerValHisGlnSerPheProAspPhe 351  
1109 ACTTTGCACTGGCAAAATATGCACATGCTCAATTAAGGGGAGA 1158  
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352 ThrPheValSerGlyGluIleLeuGlyLysPheLeuLysGlyGlu 368  
1159 CATAGATTCAAATGACGCTATTGATCTTAGCAACAAGCTTCATAGCAT 1208  
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368 uIleAspProAsnGluAlaIleAspIleCysAsnHisAlaSerLeuAlaP 385  
1209 TCTTACAAAAGCATTTAGACATTCATAAAGATTTTCATCAGTGGGACTGC 1258  
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
385 helenGlnLysHisLeuSerLeuLysArgAspPheAspLysTrpAspSer 401  
1259 TTGATTGAAGAGATGATGAGATCTTATTCAGGGGACCAACATTAC 1306  
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402 LeuValAspGlyIleGlyProAsnValIleSerGlyThrAsnIleAsp 417  
seq\_name: SwissProt\_39:PAF2\_HUMAN  
seq\_documentation\_block:  
ID PAF2\_HUMAN  
AC Q99487; O15458; PRT; 392 AA.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC  
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).  
GN PAF2H2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97115847; PubMed=8955149;  
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
RA Aoki J., Hattori M., Arai H., Inoue K.;  
RT "cDNA cloning and expression of intracellular platelet-activating  
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
RT acetylhydrolase.";

J. Biol. Chem. 271:33032-33038(1996).

RL [2]  
RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.  
RP TISSUE=Prostate;  
RX MEDLINE=98161812; PubMed=9494101;  
RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphee C.H.,  
RA Moors K., Gloger I.S., Tew D.G.;  
RA "Expression, purification and characterization of a human  
RT serine-dependent phospholipase A2 with high specificity for oxidized  
RT phospholipids and platelet activating factor.";  
RL Biochem. J. 330:1309-1315(1998).  
RN [3]  
RP REVIEW.  
RX MEDLINE=97364701; PubMed=9218411;  
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
RA "Platelet-activating factor acetylhydrolases.";  
RL J. Biol. Chem. 272:17895-17898(1997).  
CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.  
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -1- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,  
CC 3,4-DICHLOROISOCUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DPP) AND  
CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT  
CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO  
CC AMYGDALA AND FRONTAL CORTEX.  
CC -1- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.  
CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D87845; BAAL3468.1; -;  
CC EMBL; U89386; AAC39707.1; -;  
CC MIM: 602344; -;  
CC InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
CC InterPro; IPR000734; Lipase.  
CC PROSITE; PS00120; LIPASE\_SER; 1.  
KW Hydrolase; Lipid degradation.  
FT ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT CONFLICT 212 212 L -> F (IN REF. 2).  
SQ SEQUENCE 392 AA; 44035 MW; 690FB7B6F5B68317 CRC64;

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Quality: 797.00 Length: 375  
Ratio: 2.919 Gaps: 6  
Percent Similarity: 72.800 Percent Identity: 43.467

alignment\_block:

US-09-922-067-9 x PAF2\_HUMAN ..

Align seg 1/1 to: PAF2\_HUMAN from: 1 to: 392

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10 ProProValThrGlyProHisLeuValGlyCysGlyAspValMetGlu1 26  
256 TCACACTAATAGGCACCTCTCTCCGTTTATATATCCATCCCAAGATA 305  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
26 yGlnAsnLeuGlnGlySerPhePheArgLeuPheTrpProcCysGlnLys 43

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343 yrGIuGIyGluValMetValargAlametLeuAlaPheLeuGlnIys 359
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1220 CATTGAGTACCTCATAAAGATTTTGCATGGGAGCTGCTTGGATTGAAGG 1269
      |||||  |||      :::::  :::::  :::::  :::::  |||||  |||||
360 HisLeuAspLeuIysGluAspTyrAsnGlnTrpAsnAsnLeuLeuGluG 376
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1270 AGATGATCAGAACTCTATTCCAGG 1294
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376 yIleGlyProSerLeuThrProGly 384
      |      :::::  |||||

seq_name: SwissProt_39;Paf2_BOVIN
seq_documentation_block:
ID PAF2_BOVIN STANDARD: PRT: 392 AA.
AC P79106;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).
GN PAFH2
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto A.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase."
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RP REVIEW.
RX MEDLINE=97364701; PubMed=9218411;
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.N.,
RA "Platelet-activating factor acetylhydrolases."
RL J. Biol. Chem. 272:17895-17898(1997);
CC -!- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHENYL
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER
CC LOWER LEVELS IN OTHER TISSUES.
CC -!- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
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CC This SWISS-PROT entry is copyright. It is produced through a
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CC or send an email to license@isb-sib.ch).
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CC EMBL: D87559; BAA13419, 1;
CC InterPro: IPR000379; Est_lip_thioest_actsite.
CC InterPro: IPR000734; Lipase
CC PROSITE: PS00120; LIPASE_SER; 1.
CC Hydrolase; Lipid degradation..
CC ACT_SITE 236 236
CC FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILAR
CC ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILAR
CC SEQUENCE 392 AA, 43865 MW; 1DEACA2ADFACBA8 CRC64;
CC

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alignment_scores:
  Quality: 747.00      Length: 375
  Ratio: 2.798        Gaps: 6
  Percent Similarity: 71.200  Percent Identity: 41.867

alignment_block:
US-09-922-067-9 x PAF2_BOVIN ..

Align seg 1/1 LO: PAF2_BOVIN from: 1 to: 392

206 CCCCGGGGAATGGCCCTTATTCGGTTGGTTGTACAGACTAATGTTGA 255
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10 PROProValThrGlyProHisLeuValGlyCysGlyAspValMetGlu1 26
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
256 TCACACTAATAAGGCGACCTCTTGGCTTTATATTCATCCATCCCAAGATA 305
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26 yClnSerLeuGlnGlySerPhePheArgLeuPheTyrProCysGlnGlu 43
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
306 ATGATCGCCTT.....GACACCCTTTGGATCCCAATAAAGATATTTT 349
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
43 laGluThrSerGluGlnProLeuTrpIleProArgTyrGluTyrCys 59
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
350 TGGGCTCTTAGCAATTTCTTGGCAACACACTGGCTTATGGCGAACATTTT 399
    |||||:|||||:|||||:|||||:|||||:|||||:|||||
60 AlAGlyLeuAlaGluTyrLeuLysPheAsnLysArgTPrpGlyLeuLe 76
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
400 G...AGGTTACTCTTTGGTTCATGACCACTCTGCAACCTGGAATTCOC 446
    | :|||:|||||:|||||:|||||:|||||:|||||:|||||
76 uPheAsnLeuGlyValGlySerCysArgLeuProValSerTrpAsnGlyP 93
    |||:|||||:|||||:|||||:|||||:|||||:|||||
447 CTCTGAGGCCCTGGTGAATA...TATCCACTCTGTTCTTTTCTCATGTT 493
    |||:|||||:|||||:|||||:|||||:|||||:|||||
93 toPheLysThrLysAspSerGlyTyrProLeuIleIlePheSerHisGly 109
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
494 CTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTCACCTGGCATC 543
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110 MetGlyAlaPheArgThrValTyrSerAlaPheCysMetGluLeuAla 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
544 TCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTG 593
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
126 rArgGlyPheValValAlaValProGluHisArgSpGlySerAlaAla 143
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
594 CAACCTACTATTCTCAAG.....GACCAATCTGCTGCAGAA 628
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143 lathrcysPheCysLysGlnThrProGluGlnAsnGlnProAspAsnGlu 159
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629 ATAGGGGCAAGTCTTGGCTCTACCTTAGAACCCCTGAAACAA...GAGGA 675
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160 AlaLeuLysGluGluTPrIleProHisArgGlnIleGluGlyGlyGlu 176
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676 GGAGACACATATAGCAATGAGCAGGTACGGCAAGCAAGCAAGATGTT 725
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176 sGluPheTyrValArgAsnTyrGlnValHisGlnArgValSerGlyCysV 193
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726 CCCAAGCTCTCAGTCTGATTCGTGACATTCATCATGAAAGCCAGTGAAG 775
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193 alArgValLeuLysIleLeuGlnGluValThrAlaGlyGlnAlaValLeu 209
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776 AATGCATTAGATTTAAAGTTTGATATGGAACAACCTCAAGGACCTCTATCA 825
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226 pValSerArgValAlaValMetGlyHisSerPheGlyGlyIleThrAlaAl 243
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876 TTCACACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGAT 925
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243 lLeuAlaLeuAlaValGluMetGlnPheArgCysAlaValAlaLeuAsp 259
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310 LeuGlySerValHisArgSerLeuThrAspPheValPheValAlaGlyAs 326
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326 nTrpIleSerLysPhePheSerSerHisThrArgGlySerLeuAspProT 343
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1170 ATGCAAGCTATTGATCTTAGCAACAAGCTTCATTAGCATTCATTACAAAAG 1219
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343 yrGluGlyGlnGlnThrValValArgAlaMetLeuAlaPheLeuGlnLys 359
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376 yIleGlyProSerLeuThrProGly 384
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AC Q22943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLDHROLASE HOMOLOG (EC 3.1.1.47).
DE C52B9.7.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Nelson J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -1- SIMILARITY: STRONG, WITH VERTEBRATES PLATELET-ACTIVATING FACTOR
CC ACETYLDHROLASE.
CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U64598; AAK39216.1; -.
CC WormPep; C52B9.7; CE06966.
CC InterPro; IPR000379; Est_lip_thioest_actsite.
CC DR InterPro; IPR000734; Lipase.
CC PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
CC KW Hypothetical protein; Hydrolase; Lipid degradation.
CC FT ACT_SITE 326 326 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 404 404 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC SQ SEQUENCE 476 AA; 53974 MW; D61DF01F396371E9 CRC64;

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75 SerTyrlleSerSerProGlnValThrArgGlnValSer..... 88
196 AACTAAATCCCCCGGGAATGCGCCTATTCCGTTGGTTGTTACAGACT 245
89 .....GlyGlnPheGlnValGlyCysLysAspL 98
246 TAATGTTTGATCACACT.....AATAAGGCGACCTTCTTCGCTTTTA 286
98 euMetileaspGlyThrValLeuGlyAspArgGlyLeuPheMetArgLeu 114
287 TATTATCCATCCCAAGATATCATCGCTTGAC.....ACCT 324
115 TyrPheProThr....AspSerGlnAlaAlaAspLleSerSerTyrProLe 130
325 TTGGATCCCAATAAAGATAATTTTGGGCTCTTAGCAATTTCTTGA. 373
130 utrLeuProLysProGlnTyrAlaHisGlyLeuGlyGlnTyrLeuGly 147
374 ..ACACACTGGCTTATGGCAACATTTTGAGTTACTCTTTGGTTCAATG 421
147 InSerSerGlnLysMetAsnValIleThrSerThrValValGlyGlyLys 163
422 ACAACTCTGCAAAATGGAATTCCTCTGAGGCTGCT...GAAAAATA 468
164 ArgGluAspCysIleGluAsnAlaGlnMetSerThrLysCysAspLysTr 180
469 TCCACTTGTTGTTTTTCTCATGGTCTGGGCGCATTCAGGACACTTTATT 518
180 proIleValValPheSerHisGlyLeuGlyCysArgThrPheTyrS 197
519 CTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTGA 568
197 erThrTyrCysThrSerLeuAlaSerHisGlyTyrValValAlaAlaVal 213
569 CAACAC..... 574
214 GluHisLysTyrGlyLysSerGlyCysAspHisValAlaPheSe 230
575 ....AGATGATCTGCATCTGCAACTTACTATTTCAGGACCAACTCTG 620
230 rCysArgAspHisSerAlaCysTyrThrTyrGlnLeuThrGluLysAsnG 247
621 CTGCAAGAAATAGGGGACAAAGCTTGGCTCTACCTTAGAACCCGGAACAA 670
247 lyGluLeuValGlnProIleLysIleLysLeuGluLysAsnGlu 263
671 GAGGAGGACACATATACGAATAGCAGGTACGGCAAGACGCAAAAGA 720
264 LysAsnGluPheLysIleArgAsnGlnValGlyLysArgValThrG 280
721 ATGTTCCCAAGCTCTGATCTGATCTTGTGACATGATCATCGGAAG...C 767
280 uCysValLysAlaLeuAsnValLeuGluGlnLeuAsnLeuGlyThrValP 297
768 CAGTGAGCAATGCATTAGATTTAAAGTTTGTATGGAACAACCTGAAGGAC 817
297 roGluLysValLeuIleGlyAsnAspTyrAsnTrpAlaGlnPheLysAsn 313
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314 LysLeuValMetSerSerAlaSerValIleGlyHisSerPheGlyGlyAl 330
868 AACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTTCAGATGCGTATTG 917
330 aThrSerLeuAlaSerSerAlaTyrThrThrAspPheGlnLysAlaIleV 347
918 CCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATATTCACATATC 967
347 alPheAspGlyTyrMetTyrProLeuAspSerThrGlnGlnGluGlnAla 363
968 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCATATATCTCTGCTAA 1017
364 LysGlnProThrLeuPheLeuAsnValGlyAspTyrGlnTrpAsnGluAs 380
1018 TATCATAAAAATGAAAAATGCTACTCACCTGATAAAAGAAAGAAAGATGA 1067
380 nLeuAspValMetLysLysIleSerHisAsnAspGlyAsnLeuAlaL 397
1068 TTACAATCAGGGTTTCAGTCCACCAAGAAATTTTCTGCTGACTTCATTGCA 1117
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ID DAP1_YEAST STANDARD; PRT; 931 AA.
AC P33894.
DT 01-PEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE DIPEPTIDYL AMINOPEPTIDASE A (EC 3.4.14.-) (DPAP A) (YSCIV).
GN STE13 OR YC11 OR YOR219C OR YOR50-9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_taxID=4932;
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RP SEQUENCE FROM N.A.
RX MEDLINE=95066382; PubMed=7975897;
RA Anna-Arriola S.S., Herskowitz I.;
RT "Isolation and DNA sequence of the STE13 gene encoding dipeptidyl
RT aminopeptidase."
RL Yeast 10:801-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=AB320;
RA Flanagan C.A., Thorner J.;
RT "STE13."
RL Guidebook to the yeast secretory pathway, pp.1-1, Oxford university
RL Press, Oxford (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / FY1679;
RA MEDLINE=96437977; PubMed=8840505;
RA Galisson F., Dujon B.;
RT "Sequence and analysis of a 33 kb fragment from the right arm of
RT chromosome XV of the yeast Saccharomyces cerevisiae."
RL Yeast 12:877-885(1996).
CC -1- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC MATURATION OF THE
CC ALPHA-FACTOR PRECURSOR.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOME-LIKE
CC VACUOLES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE

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CC PROLYL OLIGOPEPTIDASE FAMILY. STRONG. TO DPAP B.  
 CC -----  
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DR EMBL; L21944; AAA35119.1; -;  
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 DR PIR; A49737; A49737;  
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 DR MEROPS; S09.005; -;  
 DR SGB; S0005745; STE13;  
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 DR InterPro; IPR001375; Peptidase\_S9.  
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 KW Transmembrane; Glycoprotein; Signal-anchor; Pheromone response.  
 FT DOMAIN 1 119  
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 575 TYRSEILSERLEUTHR.....ASPSETRHTRHGLINASNTH 587  
 274 CTTCCTTCGGTTATATATATCCATCCACAGATATGATCGCTTGACACC 323  
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 587 rPHEGLINSErLEuGLINSPROSErASpPHErYrASpPHEg 604  
 324 TTTGGATCCCAATAAGAAATATTTTGGGGTCTTAGCAAAATTTCTTGA 373  
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 604 luleuSerSerAlaArGTYr.....AlaIleSerLysLysLeuGly 618  
 374 ACACACTGG.....CTTATGGGCAACATTTTGGAGTTACTC..... 409  
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 619 ProAspThrProIleLysValAlaGlyProLeuThrArgValLeuAsnVa 635  
 409 ..... 409  
 635 lAlaGluIleHisAspSerIleLeuGlnLeuThrLysAspGluLysP 652  
 410 .....TTTGGTTCA 418  
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 652 heLysGluLysIleLysAsnTYrAspLeuProIleThrSerTYrLysThr 668  
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 685 aAsn.....LeuAsnProLysLysTYrProIleLeuValA 698  
 483 TTTCTCATGCTTGGGGCATTCAGGACACACTTTATCT..... 520  
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 521 .....GCTATTGGCATTGACCTGGCATCTCATGGGTT 552  
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 759 eThrGluValThrLys..... 764  
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 841 .....SerThrIleGlnAsnPheLysSerPheGluSerLeuLysArgLe 855  
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1276 TCAGAACTTTATTCAGGAGCACACATTAACACCAACCAATCAACACATCA 1325
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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.15) (PROLINE-- TRNA
DE LIGASE) (PROS).
GN PRS.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTCC 26555;
RX MEDLINE=98053570; PubMed=9392082;
RA Sentandreu M., Elorza M.V., Sentandreu R.;
RT Isolation of a putative prolyl-L-TRNA synthetase (CapRS) gene from
RT Candida albicans."
RL Yeast 13:1375-1381(1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA(PRO) = AMP +
CC PYROPHOSPHATE + L-PROLYL-TRNA(PRO).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC or send an email to license@lsb-sib.ch).
CC
DR EMBL; 086341; AAC49876.1; -
DR InterPro; IPR002106; AA-trna_ligase_II.
DR InterPro; IPR002314; trna-synt_2b.
DR Pfam; PF00587; trna-synt_2b; 1.
DR PRINTS; PR01046; TRNASYNTPRO.
DR PROSITE; PS00179; AA-TRNA-LIGASE_II_1; 1.
DR PROSITE; PS00339; AA-TRNA-LIGASE_II_2; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SO SEQUENCE 575 AA; 66209 MW; 477BE339CC4F6368 CRC64;

alignment_scores:
Quality: 100.50 Length: 262
Ratio: 0.824 Gaps: 9
Percent Similarity: 46.565 Percent Identity: 22.137

alignment_block:
US-09-922-067-9 x SYPC_CANAL
Align seg 1/1 to: SYPC_CANAL from: 1 to: 575
245 TTAATGTTTGATCACACTAATAAGCGACCTCTTGCGTTATATATATCC 294
      : |||||: |||||: |||||: |||||: |||||
258 ileYrPhetThrGluAspLysSerThrLeuIleCysAlaTyrTyrPr 274
      : |||||: |||||: |||||: |||||: |||||
295 ATCCCAAGATAATGATCGCTTCACACACCTTTGGATCCCCAATAAAA.... 340

```

```

||||| ||| ||||| ||||| ||||| |||||
274 oSer.....AsnArgValLeuGluProLysPheIleGlnAsnGluIleP 289
      : |||||: |||||: |||||: |||||: |||||
341 .....GAATATTTTGGGTCCTTAGCAAAATTTCTTGGCAACA 376
      : |||||: |||||: |||||: |||||: |||||
289 roAspIleAspLeuAspSerIleAsnAspLeuSerGluPhe.....Asn 303
      : |||||: |||||: |||||: |||||: |||||
377 CACTGGCTTATGGCAACATTTTGGAGTTTACTCTTTGGTTCAATGACAAAC 426
      : |||||: |||||: |||||: |||||: |||||
304 HisAspIleSerThrArgIleValArgIleMet..... 314
      : |||||: |||||: |||||: |||||: |||||
427 TCTTGCAAACTGGAATCCCTCTCGAGCCTGGTGAAAAATATCCACTTG 476
      : |||||: |||||: |||||: |||||: |||||
315 .....AspSerArgLeuSerSerArgSerLysPheProAspP 327
      : |||||: |||||: |||||: |||||: |||||
477 TTGTTTTTTCATGCTCTGGG.....GCATTCAGGACACATTTATTCGCT 523
      : |||||: |||||: |||||: |||||: |||||
327 heProIleSerAsnPheIleAsnArgSerLeuIleThrLeuThrAsp 343
      : |||||: |||||: |||||: |||||: |||||
524 ATTGCATTCACCTGGCATCTCATGGTTTATAGTTGCTGCTGTAGAAC 573
      : |||||: |||||: |||||: |||||: |||||
344 ileProIleValLeuAlaGlnGluGlyIleCysGlyHisCysGluG 360
      : |||||: |||||: |||||: |||||: |||||
574 CAGAGATAGATCTGCATCTGCAACTTACTATTTCAGGACCAACATCTCTG 623
      : |||||: |||||: |||||: |||||: |||||
360 uGlyLysLeuSerAlaSer.....SerAlaI 369
      : |||||: |||||: |||||: |||||: |||||
624 CAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAACCTCAACAAAG 673
      : |||||: |||||: |||||: |||||: |||||
369 leGluValGlyHisThrPheTyrLeu..... 377
      : |||||: |||||: |||||: |||||: |||||
674 GAGGAGACACATATACGAAATGACAGGTACGGCAAGACAAAGAATG 723
      : |||||: |||||: |||||: |||||: |||||
377 ..... 377
      : |||||: |||||: |||||: |||||: |||||
724 TTCCCAAGCTCTCAGTCTGATCTTGACATTGATCATGTGAAGACCCAGTGA 773
      : |||||: |||||: |||||: |||||: |||||
378 .....GlyAspLysTyrS 382
      : |||||: |||||: |||||: |||||: |||||
774 AGAATGCATTAGATTTAAAGTTTGTATATGGAACAACCTGAAGAGGACTTATT 823
      : |||||: |||||: |||||: |||||: |||||
382 eriYsProLeuAspLeuGluValAspValProThrSerAsnAsnSerIle 398
      : |||||: |||||: |||||: |||||: |||||
824 GATAGGAAAAAATACAGTAATGACATCTTTTGGTGAGCAACAGGT 873
      : |||||: |||||: |||||: |||||: |||||
399 GluLysGlnArgIleMetMetGlyCysTyrGlyIleGlySerArgI 415
      : |||||: |||||: |||||: |||||: |||||
874 TATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGTGCTATTGCCCTGG 923
      : |||||: |||||: |||||: |||||: |||||
415 eileAlaAlaIleAlaGluIleAsnArgAspGluLysGlyLeuLysTyr 431
      : |||||: |||||: |||||: |||||: |||||
924 ATGCATGGATGTTCCACTGGGTGATGAGTATATATCCAGAAATTCCTCAG 973
      : |||||: |||||: |||||: |||||: |||||
432 ProArgSerIleAlaProThrGluValThrValVal...GluValSerIy 447
      : |||||: |||||: |||||: |||||: |||||
974 CCCTCTTTTATCAACTCTGAATATATTTCCCAAT 1007
      : |||||: |||||: |||||: |||||: |||||
447 sGlnLysGlnLeuLysAsnValAsnAspAsnAsn 458
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seq_name: SwissProt_39:CLPP_CHLEU

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seq\_documentation\_block:

ID CLPP\_CHLEU STANDARD; PRT; 1010 AA.

AC P42379;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROBABLE CLPP-LIKE PROTEASE (EC 3.4.21.92) (ENDOPEPTIDASE CLP).

DE CLPP.

OS Chlamydomonas eugametos.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.







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163 ACAAGTACTGATGGCTGCTCCAGCTTGGCCAAACTAAATCCCGGG 212
109 uArgTrpAsnValThrAlaAspPheIleLysLysLysLysLysLys 122
213 GAATGGCCCTTATTCGTTGGTGTACACACTTAATGTTTGTATCACA 262
123 .....ProAlaAlaMetThrLeuGlyAsnHisGluPheAspHisThr 136
263 AATAAGGCCACCTCTTGGCTTATATATATATATATATATATATAT 312
137 ProLysGly.....LeuAlaProTyrLeuAlaGluLeuAsnLysGlu 151
313 CTTTGACACCTCTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 362
151 ylleProThrIle..... 155
363 AATTCTTTGGAACACACTGGCTTATGGGCAACATTTGAGGTACTCT 412
156 .....ValAlaAsnLeuValMet 161
413 GGTTCATGACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGA 462
162 Asn.....AsnAspProAspLeuLysSerSe 170
463 AAAATATCCA.....CTTGTGTTTTTCTCATGGCTTGGGG 500
170 rtyIleProLysSerIleLysLeuThrValGlyLysArgLysIleGly 187
501 CATTTCAGACACTTATTCCTCTATTTGGCATTTGACCTGGCATCTC 550
187 leIleGlyValLeuTyrAspLysThrHis...GluIleAlaGlnThrGly 202
551 TTTATAGTTGCT.....GCTGTAGAACACAGAFAGATCTGCATCTG 594
203 LysValThrLeuSerAsnAlaValGluAlaValArgGluAlaAla 219
595 A.....ACTT 599
219 aleuLysLysAspLysIleAspIleValValLeuSerHisCysSerT 236
600 ACTATTTTCAGGACCAATCTGCTCAGAAATAGGGAC..... 637
236 yfGluGluAspLysIleAlaAlaGluAlaGlyAspAspIleAspVal 252
638 .....AAGTCTGGCTCTACCTTGAACCCCTGGAACA 669
253 IleValGlyAlaHisSerHisSerPheLeuTyrSerProAspSerLys 269
670 ACAGAGGAG.....ACACATATAC 689
269 nProHisAspProLysAspLysValGluGlyProTyrProThrIleVal 286
690 GAAATGACAGTACGGCAA.....AGGCAAAAGAAATGTTC 727
286 luSerLysAsnLysArgLysIleProIleValGlnAlaLysSerPhe 302
728 CAA.....GCTCTCAGCTGATCTTTCAG.....ATTGA 756
303 LysTyrValGlyArgLeuThrLeuTyrPheAspAspThrGlyGluVal 319
757 TCAT.....GGAAGCCAGTCAAGAAATGATTAAGTTTGATA 800
319 nHisLysGluGlyTyrProValPheIleAspHisLysValGlnAsp 336
801 TGAACAACCTGAAGCACTTATGAT...AGGCAAAATACAGCTAAT 847
336 roGlnIleLeuLysAspLeuValProTyrArgGluLysValGluAla 352
848 GGACATCTTTTGGTGGAGCAACGGTTATTCAG.....ACTCTTAG 888
353 GlySerThrValValGlyLysThrLysIleGluLeuAspArgAspSer 369
889 TGAAGATCAGAGATTCAGATGTGGTATTCCCTCGCATGCATGTTTC 938

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369 sArgAspGlnGlyCysThrLeuGlyVal.....LeuTyrAlaAspG 383
939 CACTGGGTGATGAAGTATATTCAGAAATCTCAGCCCTCTTTTATC 988
383 lyPheAlaAspGlnTyrThrAsnAspThrPheArgProPheAlaIle 399
989 ACTCTGGAATTTCCCAATATCTCTAATATATATATATATATATAT 1038
400 GlnAlaGlyAsnPheArgAsnPro.....IleLysValGlyLysI 413
1039 CTACTCCTACCTGAT.....AAAGAAAGAAAGA 1064
413 eThrAsnGlyAspIleIleGluAlaAlaProPheGlySerThrAla 430
1065 TGATTACATCAATCAGGGTTCAGTCCACCAAGAAATTTGCTGACT 1114
430 eulleArgLeuLysGlyAlaAspIleTyrAspValAlaGluHisSer 446
1115 GCA 1117
447 Ala 447

seq_name: SwissProt_39:SVR_HELPJ

seq_documentation_block:
ID SYR_HELPJ STANDARD; PRT; 541 AA.
AC Q9ZMB9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS).
GN ARGS OR JHP0302.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX Helicobacter.
NCBI_TaxID=85963;
RN [1]
RP MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -!- CATALYTIC ACTIVITY: ATP + L-ARGININE + TRNA(ARG) -> AMP +
CC PYROPHOSPHATE + L-ARGINYL-TRNA(ARG).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; AE001467; AAD05887.1; -
CC InterPro; IPR001278; trna-synt_ld.
CC InterPro; IPR001412; trna-synt_1.
CC Pfam; PF00750; trna-synt_1g; 1.
CC PRINTS; PS01038; TRNASYNTHARG.
CC PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
FT SITE 121 129 "HIGH" REGION.
FT SITE 368 372 "KMSKS" REGION.
FT BINDING 371 371 ATP (BY SIMILARITY).

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SQ SEQUENCE 541 AA; 62158 MW; 81524A78BC125281 CRC64;

## alignment\_scores:

Quality: 96.00 Length: 294  
Ratio: 0.686 Gaps: 15  
Percent Similarity: 47.619 Percent Identity: 23.810

## alignment\_block:

US-09-922-067-9 x SYR\_HELPJ

Align seg 1/1 to: SYR\_HELPJ from: 1 to: 541

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590 TCTGCAACTTAC.....TATTTCAAGCACCATCTGCTGTCAGAAAT 630
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182 SerValThrTyProGluValPheTyLeuGluGluTyrlleLeGluIl 198
||||:|||||
631 AGGGCACAAGCTCTGG.....CTCTACCTTAGAACCTCGAAACAAGAGG 674
||||:|||||
198 eAlaLysLysAlaHisAsnAspLeuGluProSerLeuPheLysGluAsnG 215
||||:|||||
675 AGGAGACACATATACGAAATGACGAGTACGCGCAAGACGACCAAGAAATGT 724
||||:|||||
215 LuGluThrIlelle.....GluValLeuSerAspTyrlleAlaLysAspLeu 229
||||:|||||
725 TCCCAAGCTCTCAGTCTGATCTTGATCTTGATGATGGAAGCCAGTGAA 774
||||:|||||
230 .....MetLeuLeuGluIle.....LysGlyAsnLe 238
||||:|||||
775 GAATGCATTAGATTTAAAGTTTGAT.....ATGG 803
||||:|||||
238 uAspAlaLeuAspIleHisPheAspSerTyrlleAlaSerGluLysGluValP 255
||||:|||||
804 AACCACTGAAGGACTCTATT...GATAGG...GAAAAATAGCACTAATT 847
||||:|||||
255 helyshisLysAspAlaValPheAspArgLeuGluLysAlaAsnAlaLeu 271
||||:|||||
848 GGACATCTTTTGGTGGACAGCGTTATTTCACACTCTTAGTGAAGATCA 897
||||:|||||
272 TyrlleLysAspSerLysThrTrpLeuLysSerSerLeuTyrlleGlnAspG 288
||||:|||||
898 GAGATTCACATGGTGGTATGCGCTGAT...GCATGGATGTTTCACCTGG 944
||||:|||||
288 uSerAspArgValLeuLysLysGluLysAspSerTyrlleLeuAlaG 305
||||:|||||
945 GTGATGAAGTATATCCAGAAATCTCAGCCCTCTTTTATCACTACTCT 994
||||:|||||
305 LysAspIleValTyrlle.....HisAsp 311
||||:|||||
995 GAATATTTCCAAATATCTGCTGCTAATATATCAATAAATGAAAAATGCTACTC 1044
||||:|||||
312 GluLysPheGln..... 315
||||:|||||
1045 ACCTGATAAAGAAAGACAGATGATTACATCAGGGGTTTCAGTCCACCAGA 1094
||||:|||||
316 ....GlnAsnTyrlleLysTyrlleAsnIleTrpGlyAlaAspHisG 331
||||:|||||
1095 ATTTGCTGACTTCACITTTTGGCACTGGCAAAATAAATGGACAC..... 1138
||||:|||||
331 lYTyrlleAlaArgValLysAlaSerLeuGluPheLeuGlyTyrlleAspSer 347
||||:|||||
1139 .....ATGCTCAAAATTAAGGGAGACAT 1161
||||:|||||
348 SerLysLeuGluValLeuLeuAlaGlnMetValArgLeuLeuLysAsp... 363
||||:|||||
1162 AGATTCAATGACCTATGATCTTAGCAACAAAGCTTCA..... 1201
||||:|||||
364 .....AsnGluProTyrlleLysMetSerLysArgAlaGlyAsnPheIleL 378
||||:|||||
1202 .....TTAGCA 1207
||||:|||||
378 euIleLysAspValIleAspValGlyLysAspAlaLeuArgPheIle 394
||||:|||||

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1208 TTCTTCAAAAGCATTAGGACTTCATAAAGATTGTGATCAGTGGACTG 1257
||||:|||||
395 PheLeuSerLysArgLeuAspThrHisLeuGluPheAspVal...AsnTh 410
||||:|||||
1258 CTTGATTTGAAGGAGATGATGAGAACTTATTCAGGAGGACCAACATTA 1307
||||:|||||
410 rLeuLysLysGlnAspSerSerAsnProIleTyrlleHisTyrlleAla 427
||||:|||||
1308 CAACCAATCAACATCATGTTTACAGAACTCT 1339
||||:|||||
427 snSerArgIleHisThrMetLeuGluLysSer 437
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seq\_name: SwissProt\_39:CNRB\_HUMAN

## seq\_documentation\_block:

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ID CNRB_HUMAN STANDARD; PRT; 854 AA.
AC P35913;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ROD CEMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT
DE (EC 3.1.4.17) (CMP-PDE BETA).
GN PDE6B OR PDEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93351644; PubMed=8394243;
RA Khramtsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
RA Terpuhov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
RT Structural studies of its cDNA and gene.";
RL FEBS Lett. 327:275-278(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93244036; PubMed=1338685;
RA Khramtsov N.V., Feshchenko E.A., Suslova V.A., Terpuhov B.E.,
RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
RT phosphodiesterase from human retina.";
RL Bioorg. Khim. 18:1551-1554(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93247868; PubMed=1322354;
RA Collins C., Hutchinson G., Kowbel D., Riess O., Weber B., Hayden M.R.;
RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase:
RT complete retinal cDNA sequence and evidence for expression in brain.";
RL Genomics 13:698-704(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92066478; PubMed=1720239;
RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
RA Andrew S., Schappert K., Hayden M.R.;
RT "Genomic organization and complete sequence of the human gene encoding
RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
RL 4p16.3.";
RN [5]
RP Nucleic Acids Res. 19:6263-6268(1991).
RN [6]
RP VARIANT ADP TYR-557.
RX MEDLINE=93350628; PubMed=8394174;
RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
RT "Recessive mutations in the gene encoding the beta-subunit of rod
RT phosphodiesterase in patients with retinitis pigmentosa.";
RL Nat. Genet. 4:130-134(1993).
RN [6]
RP VARIANT CSNB3 ASN-258.
RX MEDLINE=94355978; PubMed=8075643;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;

```

"heterozygous missense mutation in the rod cGMP phosphodiesterase beta-subunit gene in autosomal dominant stationary night blindness."; Nat. Genet. 7:64-68(1994).

[7]

ERRATUM.

RM MEDLINE-95038845; PubMed-7951329;

RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;

RL Nat. Genet. 7:551-551(1994).

[8]

RM VARIANT ARRP ASP-576.

RM MEDLINE-96129294; PubMed-8595886;

RA Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R.,

RM Jacobson S.G., Farber D.B.;

RA "Mutations in the PDE6B gene in autosomal recessive retinitis pigmentosa.";

RM Genomics 30:1-7(1995).

[9]

RM VARIANTS ADP LYS-165; HIS-212 AND HIS-228.

RM MEDLINE-96273603; PubMed-8698075;

RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J.,

RM Jacobson S.G., Heckenlively J.H., Farber D.B.;

RA "Screening of the PDE6B gene in patients with autosomal dominant retinitis pigmentosa.";

RM Exp. Eye Res. 62:149-154(1996).

[10]

RM VARIANT ARRP ARG-699.

RM MEDLINE-96140746; PubMed-8557257;

RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,

RM Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,

RA Balget M.;

RM "A novel mutation in exon 17 of the beta-subunit of rod phosphodiesterase in two RP sisters of a consanguineous family."; Hum. Genet. 97:35-38(1996).

[11]

RM VARIANT ARRP GUN-552.

RM MEDLINE-97114306; PubMed-8956055;

RA Valverde D., Balget M., Seminago R., del Rio E., Garcia-Sandoval B.,

RM del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.;

RA "Identification of a novel R552Q mutation in exon 13 of the beta-subunit of rod phosphodiesterase gene in a Spanish family with autosomal recessive retinitis pigmentosa."; Hum. Mutat. 8:393-394(1996).

[12]

RM VARIANT ARRP ASN-535.

RM MEDLINE-98205225; PubMed-9543643;

RA Seta M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;

RM "A novel homozygous Ile535Asn mutation in the rod cGMP phosphodiesterase beta-subunit gene in two brothers of a Japanese family with autosomal recessive retinitis pigmentosa."; Curr. Eye Res. 17:332-335(1998).

CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.

CC -!- CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O = GUANOSINE 5'-PHOSPHATE.

CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA). AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.

CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.

CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF RETINITIS PIGMENTOSA (RP). RP IS A GROUP OF HUMAN DISEASES THAT LEADS TO DEGENERATION OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISUAL FIELD; AS THEIR CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISUAL FIELD AND EVENTUALLY CENTRAL VISION AS WELL. RP MAY OCCUR WITH AUTOSOMAL RECESSIVE (20-25% OF CASES; ARRP) AUTOSOMAL DOMINANT (15-20% OF CASES; ADP) OR X-LINKED (10-15% OF CASES; XRP) INHERITANCE.

CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF CONGENITAL STATIONARY NIGHT BLINDNESS (CSNB3).

CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.

CC -!- DATABASE: NAME-Mutations of the PDE6A/B/G genes;

CC NOTE-Retina International's Scientific Newsletter;

CC WWW="http://www.retina-international.com/sci-news/pdement.htm".

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CC -----

DR EMBL; S41458; AAB22650.1; -;

DR EMBL; X66142; CAA46932.1; -;

DR EMBL; X62892; CAA44569.1; -;

DR EMBL; X62893; CAA44569.1; JOINED.

DR EMBL; X62694; CAA44569.1; JOINED.

DR EMBL; X62695; CAA44569.1; JOINED.

DR PIR; A42828; A42828.

DR PIR; S34590; S34590.

DR MIM; 180072; -;

DR MIM; 268000; -;

DR MIM; 163500; -;

DR InterPro; IPR003018; GAF.

DR InterPro; IPR003607; Hdc.

DR InterPro; IPR002073; PDEase.

DR Pfam; PF01590; GAF; 2.

DR Pfam; PF00233; PDEase; 1.

DR PRINTS; PR00387; PDIESTERASE1.

DR SMART; SM00065; GAF; 2.

DR SMART; SM00471; Hdc; 1.

DR PROSITE; PS00126; PDEASE\_I; 1.

DR HydroLase; cGMP; vision; Prenylation; Lipoprotein; Membrane;

DR Retinitis pigmentosa; Disease mutation.

KW CHAIN 1 851

FT PROPEP 852 854

FT LIPID 851 851

FT VARIANT 74 74

FT VARIANT 166 166

FT VARIANT 212 212

FT VARIANT 219 219

FT VARIANT 228 228

FT VARIANT 228 228

FT VARIANT 228 228

FT VARIANT 258 258

FT VARIANT 527 527

FT VARIANT 535 535

FT VARIANT 552 552

FT VARIANT 557 557

FT VARIANT 576 576

FT VARIANT 699 699

FT VARIANT 854 854

FT CONFLICT 315 315

FT CONFLICT 320 320

FT CONFLICT 360 360

FT CONFLICT 698 698

FT CONFLICT 854 AA; 98406 MW; 76FDA6C7D73857A3 CRC64;

SQ SEQUENCE

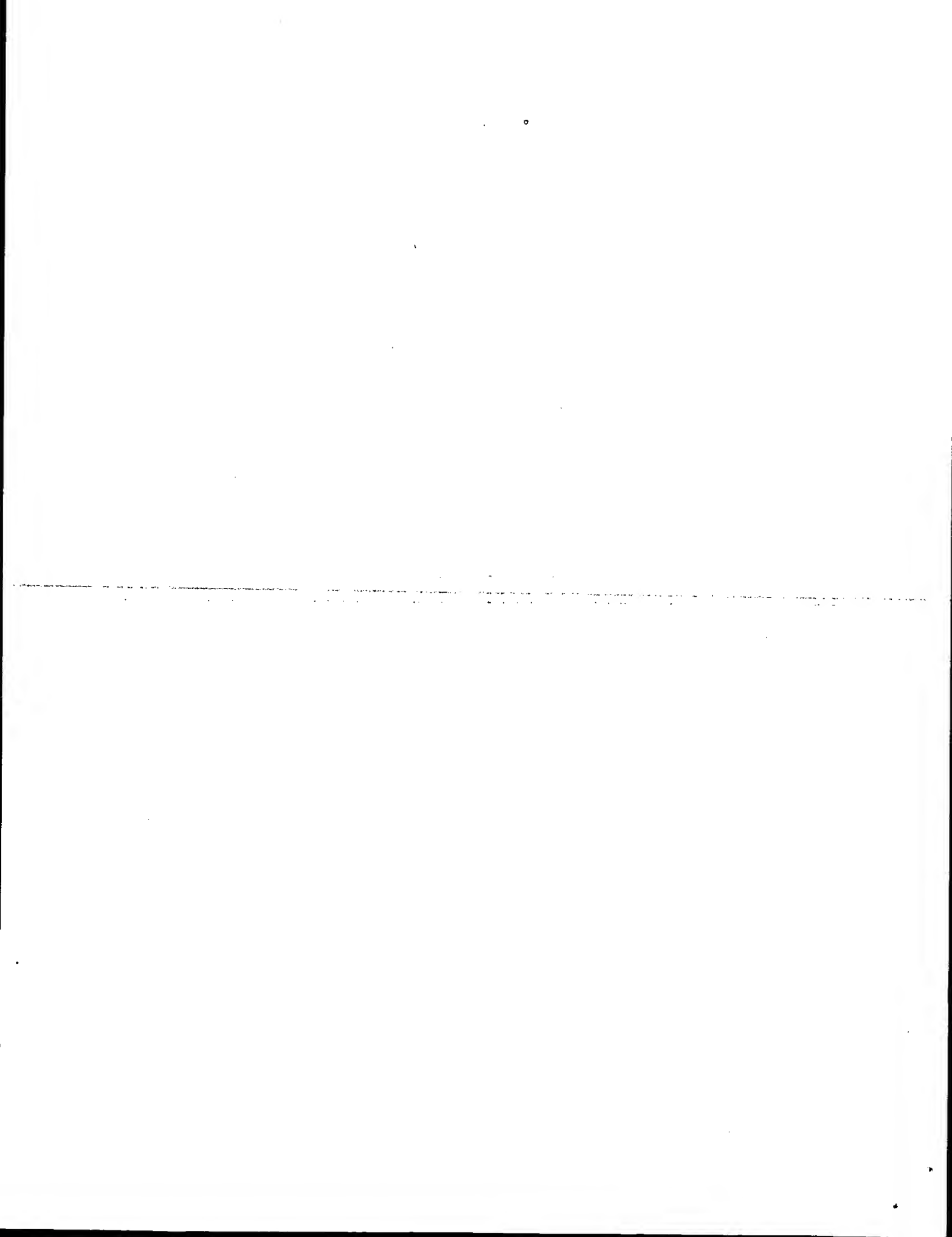
alignment\_scores: 95.50 Length: 576

Quality: 0.387 Gaps: 32

[illegible]

us-09-922-067-9.rsp

Mon Mar 11 10:02:21 2002



Sequence	Strd Orig	ZScore	EScore	Len	Documentation
sp. rodent:Q9DB74	+ 1226.50	1670.83	1.8e-36	346	! Q9db74 mus musculus (mouse). p.
sp. invertebrate:Q4753	+ 497.00	751.02	3.8e-34	384	! Q4753 caenorhabditis elegans
sp. fungi:Q9URV1	+ 295.50	440.78	6.4e-17	438	! Q9urv1 schizosaccharomyces pom
sp. bacteria:Q9KEX2	+ 249.50	369.98	5.5e-13	450	! Q9kex2 bacillus halodurans. bhd
sp. bacteria:Q9F2X9	+ 206.50	305.42	2.5e-09	386	! Q9f2x9 streptomyces coelicolor.
sp. bacteria:Q9I237	+ 162.50	234.78	1.5e-05	546	! Q9i237 pseudomonas aeruginosa.
sp. bacteria:Q9Z360	+ 149.00	217.12	0.0002	391	! Q9z360 streptomyces coelicolor.
sp. bacteria:Q9PCH9	+ 148.50	209.89	0.0003	795	! Q9pch9 xylella fastidiosa. dipe
sp. bacteria:Q56008	+ 120.50	175.52	0.0540	610	! Q56008 streptomyces sp. lipase
sp. bacteria:Q73946	+ 119.00	166.88	0.0816	322	! Q73946 synecchocystis sp. (stra
sp. bacteria:Q59798	+ 117.50	171.10	0.0971	304	! Q59798 streptomyces albus g. l
sp. archaea:Q9W211	+ 112.00	163.22	0.2836	286	! Q9w211 pyrococcus abyssi. hypo
sp. bacteria:Q47900	+ 110.50	152.62	0.4440	711	! Q47900 flavobacterium meningose
sp. archaea:Q58323	+ 110.00	153.07	0.4790	627	! Q58323 pyrococcus horikoshii. p
sp. bacteria:Q87543	+ 108.50	159.56	0.5471	232	! Q87543 capnocytophaga gingivali
sp. bacteria:Q9RK03	+ 108.50	156.66	0.5772	326	! Q9rk03 streptomyces coelicolor.
sp. bacteria:Q9ZK03	+ 106.50	155.14	0.8313	275	! Q9zkc3 chlamydia pneumoniae (ch
sp. bacteria:Q9Z1W6	+ 106.50	154.05	0.8482	310	! Q9z1w6 streptomyces coelicolor.
sp. bacteria:Q9Z1W6	+ 106.50	154.05	0.8482	310	! Q9z1w6 streptomyces coelicolor.
sp. archaea:Q9U0X6	+ 106.00	146.79	1.05	632	! Q9u0x6 pyrococcus abyssi. pep
sp. vertebrate:Q9P740	+ 105.00	142.89	1.34	820	! P97340 brachydanio rerio (zebra
sp. bacteria:Q9A405	+ 104.50	150.27	1.27	335	! Q9a405 caulobacter crescentus.
sp. bacteria:Q9KRY9	+ 104.50	141.60	1.49	868	! Q9kry9 vibrio cholerae. amino
sp. bacteria:Q9Z913	+ 103.50	139.20	1.85	955	! Q9z913 arabidopsis thaliana (md
sp. plant:Q9Z913	+ 103.50	139.20	1.85	955	! Q9z913 arabidopsis thaliana (md
sp. rodent:Q9EP61	+ 103.00	150.01	1.65	268	! Q9epm2 drosophila melanogaste
sp. invertebrate:Q9VMK2	+ 102.50	139.93	2.16	745	! Q9vmk2 drosophila melanogaste
sp. invertebrate:Q9VMK2	+ 102.50	139.93	2.16	745	! Q9vmk2 drosophila melanogaste
sp. bacteria:Q9PM89	+ 102.00	141.32	2.29	588	! Q9pm89 campylobacter jejuni. pu
sp. bacteria:Q9A4W5	+ 101.00	136.67	2.95	828	! Q9a4w5 caulobacter crescentus.
sp. fungi:Q9P778	+ 100.50	137.65	3.15	683	! Q9p778 schizosaccharomyces pom
sp. fungi:Q00302	+ 100.00	140.39	3.26	465	! Q00302 blastocladia emersoni
sp. invertebrate:Q01862	+ 100.00	140.21	3.27	474	! Q01862 caenorhabditis elegans
sp. invertebrate:Q9VTW0	+ 100.00	138.96	3.35	544	! Q9vtyw drosophila melanogaste
sp. fungi:Q14073	+ 100.00	135.52	3.57	793	! Q14073 schizosaccharomyces pom
sp. human:Q9NYU0	+ 100.00	131.84	3.82	1189	! Q9nyu0 homo sapiens (human). h
sp. rodent:Q9EP85	+ 99.00	143.87	3.62	268	! Q9ep85 calomyscus mystax (afgha
sp. bacteria:Q9CK05	+ 98.00	137.44	4.82	459	! Q9ck05 pasteurella multocida. p
sp. bacteria:Q9KLF9	+ 98.00	134.60	5.08	627	! Q9klf9 vibrio cholerae. ggde
sp. bacteria:Q74506	+ 97.50	135.22	5.46	538	! Q74506 synecchocystis sp. (stra
sp. plant:Q9ZW02	+ 97.50	129.91	6.03	964	! Q9zw02 arabidopsis thaliana (md
sp. plant:Q9ZW06	+ 97.50	129.91	6.03	972	! Q9zw06 arabidopsis thaliana (md

33 rgProSerValMetPheHisLysLeuGlnSerValMetSerAlaIaGly 49

186 TTGTGCCAACTAAATCCCGGGGAATAGGCCTTATTTCCTGTGGTG 237  
|||||:::|||||:::|||||:::|||||:::|||||  
50 SerGlyHisSerLysIleProLysGlyAsnGlySer-Tyr-ProValGlyCys 56  
238 TACAGACTTAATGTTTCATCACACTAATAAGGCACCCTTCTTCGCGTTAT 287  
|||||:::|||||:::|||||:::|||||:::|||||  
56 sThrAspLeuMetPheGlyTyrGlyAsnGluSerValPheValArgLeuT 83  
288 ATTATCCATCCCAAGATAATATGATCGCCTTGACACCCCTTTGGATCCCCAAAT 337  
|||||:::|||||:::|||||:::|||||:::|||||  
83 yrTyProAlaGlnAspGlnGlyArgLeuAspThrValTrpIleProAsn 99  
338 AAACAATATTTTTGGGCTCTACCAATTTCTTGGAACACACTGCGCTTAT 387  
|||||:::|||||:::|||||:::|||||:::|||||  
100 LysGluTyrPheLeuGlyLeuSerIlePheLeuGlyThrProSerIleVal 116  
388 GGGCAACATTTTGAGCTTACTCTTTGGTTCTCAATGACAACTCCTCGCAAAC 437  
|||||:::|||||:::|||||:::|||||:::|||||  
116 lGlyAsnIleLeuHisLeuLeutyrglySerLeuThrThrProAlaSerT 133  
438 GGAATCCCCTCTGAGGCGCTGGTCAAAAATATCCACTTGTCTTTTCT 487  
|||||:::|||||:::|||||:::|||||:::|||||  
133 rPasnSerProLeuArgThrGlyGluCysTyrProLeuIleValPheSer 149  
488 CATGCTCTGGGCATTCACAGACACTTTATCTGCTATTGGCATTCACCT 537  
|||||:::|||||:::|||||:::|||||:::|||||  
150 HisgLyLeuGlyAlaPheArgThrIleTyrSerAlaIleGlyLe 166  
538 GGCACTCATGCGCTTTATAGTTGCTGCTCTAGAACACAGACATAGACTG 587  
|||||:::|||||:::|||||:::|||||:::|||||  
166 uAlaSerAsnGlyPheIleValAlaThrValGluHisArgAspArgSerA 183  
588 CAYCTCGAATCTACTATTTCACAGGACCATACTGCTGCAGAAATAGGGAC 637  
|||||:::|||||:::|||||:::|||||:::|||||  
183 laSerAlaThrTyrPhePheGluAspGlnValAlaLaLysValGluAsn 199  
638 AAGTCTTGGCTCTTACCTTAGAACCTCTGAACAGAGAGAGAGACACATAT 687  
|||||:::|||||:::|||||:::|||||:::|||||  
200 ArgSerTriLeuTyrLeuArgLysValLysGlnGluGluSerGluSerVa 216  
688 ACCAAATGAGCAGGTACGCCAAGAGCAAAAGAATGTTCACAGCTCTCA 737  
|||||:::|||||:::|||||:::|||||:::|||||  
216 lArgLysGluGlnValGlnGlnArgAlaIleGluCysSerArgAlaLeus 233  
738 GTCTGATCTTCACATTTGATCATGCGAAAGCAGTCAGAAATTCATAGAT 787  
|||||:::|||||:::|||||:::|||||:::|||||  
233 erAlaIleLeuaspIleGluHisGlyAspProLysGluAsnValLeuGly 249  
788 TTAAAGCTTTGATATCGAACACTGAAGCACHCTATTGATAGGGAAAAAT 837  
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250 SerAlaPheAspMetCysGlnLeuLysaspAlaIleAspGluThrLysIl 266  
838 AGCAGTAATTTGACATCTTTTGTGGAGCAACGCTTATTTCAGACTCTTA 887  
|||||:::|||||:::|||||:::|||||:::|||||  
266 eAlaLeuMetGlyHisSerPheGlyGlyAlaThrValLeuGlnAlaLeus 283  
888 GTCAAGATCAGAGATTACAGATGTGGTATTCGCCCTGGATGATCGATCTTT 937  
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283 erGluAspGlnArgPheArgCysGlyValAlaLeuAspProTrpMetTyr 299  
938 CCACGTGGGTGATGAAGTATATTCAGAAATTCCTCAGGCCCTCTTTTAT 987  
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300 ProValAsnGluGluLeuTyrSerArgThrLeuGlnProLeuLeuPheIl 316  
988 CAACCTCTGAATATTTCCAATATCTGCTTAATATCATATAAATCAAAAT 1037  
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316 eaSnSerAlaLysPheGlnThrProLysAspIleAlaLysMeLysLysp 333  
1038 GCTACTCACCTGATAAAGAAAGAAGATGATTACAATCAGG 1078  
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333 heryrGlnProAspLysGluArgLysMetIleThrIleLys 346

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seq_name: sp_invertebrate:O44753

seq_documentation_block:
ID O44753 PRELIMINARY; PRT; 384 AA.
AC O44753;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE W03G9.6 PROTEIN.
GN W03G9.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
OC [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnson M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan J., Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Smailton S., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston A., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome elegans.";
RT RT
RL Nature 368:32-38(1994).
RN [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Dante M., Keppler D.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston J.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF039716; AAB96738.1;
DR InterPro: IPR000379; EST_clip_thioest_actsite.
SQ SEQUENCE 384 AA: 42888 MW: FDCFI1F97C162657C CRC64;

alignment_scores:
Quality: 497.00 Length: 348
Ratio: 2.097 Gaps: 9
Percent Similarity: 68.103 Percent Identity: 33.908

alignment_block:
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14 LysMetPro.....GlyGlnPheIysValGlyCysMetAspLeu 27

250 GTTTTGATCAG...ACTAATAAGGCGACCTCTCTGCGTTTATATCCAT 296
||||:||||| :|||:||||| ||||| ||||| |||||
27 tIleGluGluAlaAlaGlySerGlyLeuPheMetArgLeuPhePhePro 44

297 CCCAAGATGAATGATGCCTTGAC.....ACCTTTGGATCCCA 334
||| :||||:
44 hr...AspSerGluIleThrGlyProSerSerLeuProValTrpIlePro 59

335 AATAAAGATATATTTTGGCGCTTACGAAATTTCTTGGAA...ACACACTG 381
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60 ArgProGluTyrAlaTyrGlyValGlyGluTyrLeuGlyHisSerProH 76

```



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382 GCTTATGGGCAACATTTGAGGTTACTCTTTGGTTCAATGACAACTCTG 431
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76 sGlnMetAspLeuIleSerSerLeuValIleGlyAspLysArgValAspC 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
432 CAAACTGGAATTCCTCCCTG...AGGCCTGGTGAATAATATCCACTTGT 478
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
93 ySleAspAsnAlaGlnLeuSerThrLysSerAspLysTrpProValLeu 109
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
479 GTTTTTTCTCATGGCTTGGGCATTCAGGACACTTTATTCTGCTATGG 528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
110 ValPheSerHisGlyLeuGlySerArgThrPheTyrSerThrTyrCy 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
529 CATTGACCTGGCATCTCATGGGTTTATAGTTGCTGTAGAACACAGAG 578
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
126 sThrSerLeuAlaSerHisGlyTy-VaIValAlaAlaValGluHisArg 143
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
579 ATAGATCTGCATCTGCACTTACTATTCAAGGACCAATCTGCTGCAGAA 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 spSerSerAlaCysTrpThrTyrLysLeuValGluLysAsnGlyThrLeu 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
629 ATAGGGGACAAGTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGGAGA 678
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
160 ValGluLysProMetLysIleLysLeuValAspArgAsnAspLysAspGI 176
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
679 GACACATATACGAAATGACAGCTACGCGCAAGAGCAAAAGAAATGTTCC 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
176 nPheLysIleArgAsnGluGlnValGlyArgAlaGluGluCysAlaL 193
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729 ANGCTCTCATGCTTATCTTGATTCATGTGATGGAAGCCAGTGAAGAA 778
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193 ySAlaValLysIleLeuGluGlnLeuAspSerGlyAsn...ValLysAsp 208
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779 GCATTAGATT...AAGTTTGATGTGAACACACTGAGGAGCTCTAT 822
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209 LysValIleIleGlyAsnAlaAsnAlaLeuGluPhePheLysAsnLysLe 225
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
823 TGATAGGAAAAAATAGCAGTAATTTGGACATCTTTTGGTGAGCAAGG 872
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
225 uLeuThrThrAlaSerIleIleGlyHisSerPheGlyGlyAlaThrS 242
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
873 TTATTCAGACTCTTACTGAAGATCAGAGATTCAGATGTGGTATTCCTCG 922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
242 erIleAlaSerSerSerAsp.....PheGlnLysAlaIleValLeu 256
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
923 GATGATGATGATTTCCACTGGCTGATGAAGTATATTCGAATTCCTCA 972
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
257 AspGlyTrpMetTyrProLeuAspGlnAsnGlnGlnGluAlaLysGI 273
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
973 GCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTAATATCA 1022
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 nProIleMetPheLeuAsnValGlyAspTrpGlnTrpAsnGluAsnLeuG 290
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1023 TAAAAATGAAAAATGCTACTACCTACCTGATAAAGAAAGAAAGATTTACA 1072
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
290 luValMetArgLysIleLeuProAsnAsnGluGlyAsnIleLeuLeuThr 306
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1073 ATCAGGGGTTTCAGTCCACCAAGATTTTGTGCTGACTTCACTTTGGCACTGG 1122
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 LeuSerGlyAlaValHisGlnSerPheThrAspPheProPheValPhePr 323
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1123 CAAAAATATTTGGACATGCTCAAAATTAAGGAGACATAGATTTCAATG 1172
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
323 oAsnTrpLeuAlaLysGlnPheGlyValHisGlyProThrGluProTyrL 340
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1173 CAGCTATTGATCTTAGCAACAAGCTTCATTTAGCATTCCTTACAA 1216
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
340 euCysMetGlnSerAlaIleGluLeuThrLeuSerPheLeuLys 354
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seq\_name: sp\_fungi:Q9URV1

seq\_documentation\_block:

ID Q9URV1

PRELIMINARY;

PRT: 438 AA.

AC Q9URV1;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHELICAL 49.8 KDA PROTEIN C106.11C IN CHROMOSOME II.
GN SPBC106.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Rajandream M.A., Barrell B.G., Davis P., Churcher C.M.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: PARTIAL with OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
EMBL: AL110295; CAB53727.1; -.
DR Hypothetical protein
KW
SQ SEQUENCE 438 AA; 49847 MW; 24767654F94C10F9 CRC64;

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## alignment\_scores:

Quality: 295.50 Length: 452

Ratio: 1.274 Gaps: 22

Percent Similarity: 51.327 Percent Identity: 24.779

## alignment\_block:

US-09-922-067-9 x Q9URV1 ..

Align seg 1/1 to: Q9URV1 from: 1 to: 438

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10 GlnLeuProAlaTyrCysGlyProLeuProValGlySerLeuValLeuGI 26
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 .....TGTACAGACTTAATGTTGTATGCACACA 260
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26 uLeuSerValProGluGluPheArgCysGluTyrLysThrIleGluHisL 43
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261 CTAATAAGGGGACACCTCTTGGCTTATATATAT.....CCATCCCAA 301
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43 ySLeuArgThrValLysValArgIlePheTyrProLeuAspProThrLys 59
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302 GAT...AATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATT 348
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60 AspValGluProArgThrAspGluLeuTrpLeuProPheHisGluGlyII 76
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349 TTGGGCTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGCAACATTT 398
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76 eProGluValAlaLys.....GlyPheArgTrpTrp.....LeuL 88
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
399 TGAGGTACTCTTTCGTTCAATGACAACTCTGCAAACTGGAATTCCTCT 448
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88 euArgAlaPheAlaSerGlyLeuThr.....AsnLeuAlaLeuPro 101
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449 CTGAGCGCTGGTGAA.....AAATATCCACT 474
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
102 ValTyrLysGlyGluLeuPheHisProProAsnAsnGlyLysLeuProva 118
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
475 TGTGTTTTTTCTCATGGCTTGGGGCATTCAGGACACTTTATTCTCTCTA 524
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
118 lPheIlePheSerHisGlyLeuValGlySerArgAsnValTyrSerSerL 135
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525 TTGGCATTCACCTGGCATCTCATGGGTTTATAGTTGCTGTAGAACAC 574
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135 euCysGlyThrIleAlaSerTyrGlyIleValValLeuAlaMetGluHis 151
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
575 AGAGATAGATCTGCA..... 589
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
152 ArgAspAsnSerAlaIleIleSerThrValArgAspProLeuHisProGI 168
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
590 .TCTGCAACTTACTATTTCAGGAGCAATCTGCTGCAGAAATAGGGACA 638
    : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

seq\_name: sp\_bacteria:O9KEX2







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731 GCTCTCAGTCTGATTTCTTGACATTGATCATGGAAGCCAGTGAAGATGC 780
    : : : : :
212 ValAlaAla.....:ThrArgAl 217
781 ATTAGATTAAAGTTTCATATGAGACACTGAGGACTCT.....820
    : : : : :
217 aAlaAspLeuArgValArgGluArgLeuLeuArgSerProGlyAlaV 234
821 .....ATTGATAGGGAATAATAGCAGTAATTTGGACATTCT 856
    : : : : :
234 aGlyLeuProArgLeuAspProSerArgValAlaValGlyHisSer 250
857 TTTCGTGGACCAAGGTTTATCAGACTCTTAGTGAAGACAGATTCAG 906
    : : : : :
251 MetGlyGlyAlaAlaPheGluAlaLeuArgThrAspAlaGlyPheAl 267
907 ATGTGGTATTGCCCTGGATCGATGGATGTTTCCACCTGGGTGATGAAGTAT 956
    : : : : :
267 aAlaAlaAsnLeuAspGlyThrValHisThrGlyGly.....A 281
957 ATTCCAGATTCTCAGCCCTCTTTTATCAACTCT...GAATATTC 1003
281 rgSerProValAspArgProPheLeuLeuGlyAlaGlyGluHisGly 297
1004 CAATATCTCTCTAATATCATATAAAATCAAAATGCTACTCACTGATAA 1053
    : : : : :
298 ArgProGlyAlaAspProThrTrpGlnArgAlaTrpArgAspLeuSerGl 314
1054 AGAAGAAAGATCATATACATCAGGGTTCAGTCCACAGAAATTTGCTG 1103
    : : : : :
314 YProArgTrpLeuSerValArgGlyAlaGlyHisLeuSerPheThrA 331
1104 ACTTCACTTTTGGCACTGGCAATAATTTGGACATGCTCAAAATTAAG 1153
    : : : : :
331 spTyr.....AlaArgLeuLeuGluArgThr 339
1154 GGAGACATAGATTCAATGACGCTATTGAT.....CT 1185
    : : : : :
340 GlyThrAlaGlyGluValThrLeuGlyAlaAlaAspAlaGlyArgVa 356
1186 TAGCAACAAAGCTTCAATTAGCATTTCTTACAAAGCATTTA 1225
    : : : : :
356 lThrArgGluValValAlaPheLeuAspGluArgLeu 369
seq_name: sp_bacteria:Q9PHC9
seq_documentation_block:
ID Q9PHC9 PRELIMINARY; PRT; 795 AA.
AC Q9PHC9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DIPEPTIDYL-PEPTIDASE.
GN XF0015.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP STRAIN=9A5C;
RC MEDLINE=20365717; PubMed=10910347;
RX Simpson A.J.G.; Reinach F.C.; Arruda P.; Abreu F.A.; Acencio M.;
RA Alvarenga R.; Alves L.M.C.; Araya J.E.; Baia G.S.; Baptista C.S.;
RA Barros M.H.; Bonaccorsi E.D.; Bordin S.; Bove J.M.; Briones M.R.S.;
RA Bueno M.R.P.; Bonaccorsi A.E.; Camargo L.E.A.; Carraro D.M.; Carrer H.;
RA Colauto N.B.; Colombo C.; Costa F.F.; Costa M.C.R.; Costa-Neto C.M.;
RA Coutinho L.L.; Cristofani M.; Dias-Neto E.; Docena C.; El-Dorry H.;
RA Facincani A.P.; Ferreira A.J.S.; Ferreira V.C.A.; Ferto J.A.;
RA Fraga J.S.; Franca S.C.; Franco M.C.; Frome M.; Furian L.R.;
RA Garnier M.; Goldman G.H.; Goldman M.H.S.; Gomes S.L.; Gruber A.;
RA Ho P.L.; Hohnselt J.D.; Junqueira M.L.; Kemper E.L.; Kitajima J.P.;
RA Krieger J.E.; Kuramae E.E.; Laigret F.; Lambais M.R.; Leite L.C.C.;

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RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marck C.F.M., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Monteiro-Vitorello C.B.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003856; AAF82828.1; -.
DR InterPro; IPR000379; BPD_transp.
DR InterPro; IPR001375; Est_lip_thioest_actsite.
DR Pfam; PF00326; Peptidase_S9; 1.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBR; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 795 AA; 91075 MW; ECEID9F3D51C5777 CRC64;

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## alignment\_scores:

Quality: 148.50 Length: 327  
Ratio: 1.046 Gaps: 16  
Percent Similarity: 43.425 Percent Identity: 21.101

## alignment\_block:

US-09-922-067-9 x Q9PHC9 ..

Align seg 1/1 to: Q9PHC9 from: 1 to: 795

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359 AGCAAAATTTCTTGGACACACACTGGCTTATGGCAACATTTTGAGTTA.. 406
    ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
528 SerThrPheLysAlaLysGlnTrpIleGlnProGluTyrValGlnIlePr 544
407 .....:CTCTTGGTTCANTGACACACTCTCGCAA 434
    : : : : : : : : : : : : : : : : : : : : : : : :
544 oSerLysHisGlyAlaGlyValIleTrpGlyLysTyrTyrGlyProAlas 561
435 ACTGGAATTCCTCTCAGGCTGGTGAAATAATATCCACTGTGTGTTTT 484
    : : : : : : : : : : : : : : : : : : : : : : : :
561 er.....LeuGlnProGluLysArgTyrProIleValMetPhe 573
485 TCTCATGGTCTTGGGCAATTCAGGACACTTTATTCTGCTATTGGCAATTGA 534
    ||||| ||| : : : : : : : : : : : : : : : : : : : :
574 ValHisGlyAlaGlyTyrLeuGlnAsnVal..... 583
535 CCTGGCATCTCATGGGTTTATAGTTCTGCTGTAGAACACAGAGATAGAT 584
584 .....:S 584
585 CTGCATCTGCACTTACTATTTCAGGACCACTCTCTGCAGAAATAGGG 634
    ||||| : : : : : : : : : : : : : : : : : : : :
584 erAlaArgTyrProSerTyrPheArgGluGln..... 594
635 GACAAGTCTTGCTCTACCTTGAACCCCTGAACACAGAGAGGAGACACA 684
    : : : : : : : : : : : : : : : : : : : : : : : :
595 .....MetPheHisThrLeuLeuValGlnLysGly..... 604
685 TATACGAATGACGACGTACGGCAAGCAAAAGATGTTCCCAAGCTC 734
604 ..... 604
735 TCAGTCTGATCTTTCGACATTGAT.....CATGGAAG 766
    : : : : : : : : : : : : : : : : : : : : : : : :
605 ..TyrIleValLeuAspLeuAspTyrArgAlaSerAlaGlyHisGlyArg 620

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KW Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 48
FT CHAIN 49 310 LIPASE.
FT ACT_SITE 179 179 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 310 AA: 32649 MW: 485810BA649AD86 CRC64;

alignment_scores:
  Quality: 120.50 Length: 373
  Ratio: 0.925 Gaps: 12
  Percent Similarity: 39.142 Percent Identity: 16.622

alignment_block:
US-09-922-067-9 x Q56008 ..
Align seg 1/1 to: Q56008 from: 1 to: 310

203 ATCCCCCGGGAATGGCTATTATCCGTTGGTTGTACA.....GA 243
    ||| :::::::::::::::::::: |||
54 IleGluAlaSerArgGlyProTyrAlaThrSerGlnThrSerValSerSe 80

244 CTTAATGTTTGATCACACATNAAGCGACCTCTTCGTTATATATATC 293
    |||::: :: :: |||||
80 rLeuValAlaSerGlyPheGlyGlyThr.....IleTyrTyrP 94

294 CATCCCAAGATAATGATGCGCTTGACACCGCTTGGATCCCAATAAGAA 343
    |||
94 rThrSerThrAlaAsp..... 99

344 TATTTTTGGGGCTTACCAAAATTTCTGGACACACTGGCTTATGGCAA 393
    |||||
100 .....GlyThr..... 101

394 CATTTTGAGTTTACTCTTTGGTTCAATGACAACTCTCGAACTGGAATT 443
    |||||:::
102 .....PheGlyAla..... 104

444 CCCCTCTGAGGCCGNGGAAANAATATCCACTTCTGTTTTTTCATGCT 493
    |||||:::|||||
105 .....ValValIleSerProGly 110

494 CTTGGGGCATTCAGACACATTTATCTGTTATGGCAATGACCTGGCATC 543
    :: |||||::: :: :: |||||
111 PheThrAlaTyrGlnSerSerIleAlaTyrLeuGlyProArgLeuAlaSe 127

544 TCATGGGTTTATAGTCTGCTGTAGAACACAGATAGATCTGCATCTG 593
    |:|||||::: ||| ::::: ::
127 rGlnGlyPheValValPheThrIleAspThrAsn..... 138

594 CAACTTACTATTTCAGGACCAATCTGCTCCAGAAATAGGGACAACTCT 643
138 ..... 138

644 TGGCTCTACCTTAGAACCCGTAACAAAGAGGAGGAGACATATACGAA 693
    ||||| ||| ::
139 .....ThrThrLeuAspGlnProAsp..... 145

694 TGACGAGTACGGCAAGACAAAGAAATGTTCCCAAGCTCTCAGTCTCA 743
145 ..... 145

744 TTCTTGACATTGATCATGGAAAGCCACTGAAGAATGCATTAGATTTAAAG 793
    :::::||||: :: :: |||||
146 .....SerArgGlyArgGlnLeuLeuSerAlaLeuAspTyrLeu 158

794 TTTGATATGGAACACTGAAGGACTCTTCTCATTAGGGAANAATACACT 843
    :: ::::::::::: |||
159 ThrGlnArgSerSerValAlaTyrArgValAspAlaThrArgLeuGlyIva 175

844 AATTGGACATCTTTTGGTGGACGACAGCGTTATTCAGACTCTTAGTGAAG 893
    |:|||||::: |||||::: :: :: |||||
175 lMetGlyHisSerMetGlyGlyGlySerLeuGluAlaAlaLysSerA 192

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...
481 PropheValLeuGluGlnAlaArgSerPheProArgLeuAlaSerArgAs 497
1216 AAAGCATTTAGGACTT .....CATAAAGATTTTTGATCAGT 1250
497 pLysTyrLeuThrLeuMetGluGlyGlnAlaHisValAspPheSerLysI 514
1251 GGGACTGCTGATTGAAGGAGATGATGAGAAATCTT ..... 1285
514 leAspAlaAsnIleLysAsnValValGluSerValGluAlaValSerLeu 530
1286 ....ATTCCAGGAGCAAC...ATTAAACCAACCAATCAACACATCATGTT 1329
531 LysLeuProAspProAsnLeuLeuHisThrTyrGlySerAlaValMetVa 547
1330 A 1330
547 I 547

seq_name: sp_bacteria:Q59798
seq_documentation_block:
ID Q59798 PRELIMINARY; PRT; 304 AA.
AC Q59798;
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LIPASE PRECURSOR (BC 3.1.1.3) (TRIACYLGLYCEROL LIPASE).
GN LIP.
OS Streptomyces albus g.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299159; PubMed=8026751;
RA Cruz H., Perez C., Wellington E., Castro C., Servin-Gonzalez L.;
RT "Sequence of the Streptomyces albus G lipase-encoding gene reveals the
RT presence of a prokaryotic lipase family.";
RL Gene 144:141-142(1994).
CC -1- CATALYTIC ACTIVITY: TRIACYLGLYCEROL + H(2)O -> DIACYLGLYCEROL + A
CC FATTY ACID ANION.
CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
DR EMBL; U03114; AAA53485.1; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 304 LIPASE.
FT ACT_SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 304 AA; 31984 MW; F2CA16ABD1AF2AB2 CRC64;

alignment_scores:
. Quality: 117.50 Length: 371
. Ratio: 0.778 Gaps: 11
Percent Similarity: 40.701 Percent Identity: 17.790

alignment_block:
US-09-922-067-9 x Q59798 ..
Align seg 1/1 to: Q59798 from: 1 to: 304

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55 ArgAlaSerIleGluAlaProArgGlyProTyrAlaValSerGlnThrSe 71
242 .....GACTTAATGTTGATCACACTAATAAGGCGACCTTCITGGCGTT 284
71 rValSerSerLeuValSerGlyPheGlyGlyThr.....I 85
285 TATATTATCATCCCAAGATATGATCGCTTGACACCCCTTGGATCCA 334

```

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...
85 lefTyrProThrSerThrGlyAsp..... 93
335 AATAAAGAATATTTTGGGGCTCTAGCAAAATTTCTTGAACACACTGGCT 384
94 .....GlyThr..... 95
385 TATGGGCAACATTTTCAGGCTTACTCTTTGGTTCAATGACAACCTCTGCAA 434
96 .....PheGlyAla..... 98
435 ACTGGAATTTCCCTCTGAGGCTGTGGAATAATATCCACTTGTGTTT 484
99 .....ValValVal 101
485 TCTCATGCTTGGGCACTTCAGGACACTTTATCTGCTATTGGCAATTGA 534
102 ThrProGlyPheThrAlaThrGluSerSerMetAlaTrpLeuGlyProAr 118
535 CCTGGCATCTCATGGGTTTATAGTCTGCTGTAGAACACAGATAGAT 584
118 gLeuAlaSerGlnGlyPheValValPheThrIleAsp..... 130
585 CTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGG 634
130 ..... 130
635 GACAAGTCTGGCTCTACCTTAGAACCTCAACACAGAGAGGACACACA 684
131 .....ThrLeuThrThrLeuAspGlnProAsp..... 139
685 TATACGAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTC 734
139 ..... 139
735 TCATCTCTGATCTTGACATTGATCGAAGCCAGTGAAGATGCATTA 784
140 .....SerArgGlyArgGlnMetLeuAlaAlaLeu 149
785 CATTAAAGTTTGATATGGAACCACTGAAGGACTCTATTGTATAGGAAAA 834
150 AspTyrLeuThrGluArgSerSerAlaArgThrArgIleAspGlyThrAr 156
835 AATGACAGTAATTCGACATTCCTTTGGTGAGCAACGGTTATTTCACACTC 884
166 gLeuGlyValIleGlyHisSerMetGlyGlyGlyThrLeuGluAla 183
885 TTAGTGAAGATCAGAGATTCAGATGTGCTATTGCCCTGGATGCATGGATG 934
183 laLysSerArgProSerLeuLysAlaAlaIleProLeuThrProTrpAsn 199
935 TTTCCACTGGGTGATGAAGTATATCCAGAAATCCCTCAGCCCTCTTTT 984
200 Leu.....AspLysThrTrpProGluValThrThrProThrLeuVa 213
985 TATCAACTCTGAATATTTCCAAATATCCTGCTAATATATCAATAAAATGAAA 1034
213 lValGlyAlaAspGlyAspThrValAlaProValAlaThrHisAlaLysP 230
1035 AATGCTACTACCTCATTAACAAAGAGATGATTACAATCAGGCTTCA 1084
230 roPheTyrSer.....SerLeuProSerSer 238
1085 GTCCACCAGAAATTTTGTGCTGACTTTCCTTTCGAACTGGCAAAATAATGG 1134
239 ThrAspArgAlaTyrLeuGluLeuAsnAsnAlaThr..... 250
1135 ACACATGCTCAATTAAGGAGACATAGATTCAAAATGACGCTATTGATC 1184
251 .....HisPheAlaProAsnL 256
1185 TTAGCAAC.....AAAGCTTCATTAGCAATTCATTACAAAGCAT 1222

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550  GTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACT 599
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109  y.....
600  ACTATTTC AAGGCAACAATCTCTCGCAAAATAGGGACAAGCTTCGGCTC 649
      ::::  |||  ::  ||| ||| |||
110  .... GluSerGluCluYSerLysThrThrIleGlyAsp..... 120
650  TACCTTTAGAACCCGTGAACAACAGAGGAGGACACATATACGAAATGAGCA 699
      ::::  |||  ::  ||| ||| |||
120  .....
700  GGTACGGCAAAAGAGCAAAAGAAATCTTCCCAAGCTCTCAGTGTGTTGT 749
      ::::  |||  ::  ||| ||| |||
120  .....
750  ACATTGTATCATGGAAGCCAGTGAAGAAATCCATTACATTTAAAGTTTGAT 799
      ::::  |||  ::  ||| ||| |||
121  .... LysGluIleLeuAspLysSerGlyAla 129
800  ATGGAACACTGAAGGACTCTATGTAGGGAAAAATAGCACTAATTTGG 849
      ::::  |||  ::  ||| ||| |||
130  IleAspTrpLeuLeuSerAsnThrAsnThrLysLysIleAlaLeuIleGlu 146
850  ACATTTCTTTTGGTGGAGCAACGGTTATTCCAGACTCTTGTAGTGAAGATCAGA 899
      ::::  |||  ::  ||| ||| |||
146  yPheSerMetGlyAlaMetValThrIleArgAlaLeuAlaGluAspGluAla 163
900  GATTTCAGATGUGGTATTGGCTCGGATGCATGGATGTTTCCACTGGGTGAT 949
      ::::  |||  ::  ||| ||| |||
163  rGValCysCysGlyIleAlaAspSerProProIleTyrIle.....Asp 177
950  GAATCATATTCCAGAAATCTCTCAGCCGCCCTCTTTTATTCAACTCTGAATA 999
      ::::  |||  ::  ||| ||| |||
177  LysThrGlyAlaArgGlyLeuLys.....TyrPheAlaAsnLeuProGlu 192
0000  TTTTCCAATATCTTCGTAATATCATATAAA...ATGAAAAAATGCTACTCAC 1046
      ::::  |||  ::  ||| ||| |||
192  uPheLeuTyrPro.....IleIleLysProPheThrLysMetPheSer 207
CTGATTAAGAAACAAGATGATTCAATCAGGGGGTTTCAGTCCACCAG 1093
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207  LyAlaLysGluAlaAsnIleIleAspTyrAlaAspLysValArgLys 222

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seq_documentation_block:
  ID Q47900 PRELIMINARY; PRT; 711 AA.
  AC Q47900;
  DT 01-NOV-1996 (TrEMBLrel. 01, Created)
  DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
  DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
  DE DIPEPTIDYL PEPTIDASE IV.
  OS Flavobacterium meningosepticum.
  OC Bacteria; CF8 group; Flavobacteria; Flavobacteriaceae;
  OC Chryseobacterium.
  NCBI_TaxID=238;
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=95314307; Pubmed=7793970;
  Kabashima T., Yoshida T., Ito K., Yoshimoto T.;
  "Cloning, sequencing, and expression of the dipeptidyl peptidase IV gene from Flavobacterium meningosepticum in Escherichia coli." Arch. Biochem. Biophys. 320:123-128(1995).
  EMBL; D42121; BAA07702.1;
  MEROPS; S09_013;
  InterPro; IPR002469; DPPIV_N_term.
  InterPro; IPR000379; Est_lip_thioest_actsite.
  InterPro; IPR001375; Peptidase_S9.
  InterPro; IPR002471; Prol_endopep_ser.
  Pfam; PF00930; DPPIV_N_term; 1.
  Pfam; PF00326; Peptidase_S9; 1.

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RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.;

RL DNA Res. 5:55-76(1998).

DR EMBL; AF000002; BAA25683.1; ..

DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.

KW Hypothetical protein; complete proteome.

SQ SEQUENCE 522 AA; 73231 MW; 6D4BAB1A12614E02 CRC64;

alignment\_scores:

Quality:	110.00	Length:	290
Ratio:	0.932	Gaps:	14
Percent Similarity:	40.690	Percent Identity:	20.345

alignment\_block:

US-09-922-067-9 x 058323 ..

Align seg 1/1 to: 058323 from: 1 to: 622

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344 TATTTTGGGGT.....CTAGCAAAATTTCTGGACACA 378
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287 TyrLeuTrpAspGlyGluValArgGluIleAlaLys.....GlyLysH 301
379 CTGGCTATGGC.....AACATTTTGAGGTTACTCTTTGGTT 416
|||||
301 strPileMetGlyPheAspAlaAspGluArgLeuIleTyrLeuLysGluT 318
417 CAATGACAACCTCTGCAAAAC.....TGGAATTC 445
:: ||| |||||:: |||||::
318 hralathrArgProAlaGluLeuTyrLeuTrpAspGlyGluGluArgGln 334
445 ..... 445
335 LeuThrAspTyrAsnGlyLeuIlePheLysLysLeuLysThrPheGluPr 351
445 ..... 445
351 oArgHisPheArgPheLysSerIleAspLeuGluLeuAspGlyTrpTyrI 368
446 .....CTCTGAGGCTGGTGAATAATATCCACTTGTCTGTTTCT 487
|||||
368 IeLysProGluIleLysGluGlyGluLysAlaProValIleValPheVal 384
488 CARGGT.....CTTGGGCAATTCAGGACACTTTATCTGCTATTGGCAT 531
|||||
385 HisGlyGlyProLysGlyMetTyrGlyTyrTyrPheLysTyrGluMetGl 401
532 TGACCTGGCATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGATA 581
|||||
401 nLeuMetAlaSerLysGlyTyrTyrIleValTyrValAsnProArgGlys 418
582 GATCTGCATCTGCACTTACTATTTCAGGACCAATCTGCTGCAGAAATA 631
|||||
418 exAsnGly.....TyrSerGluAsp..... 424
632 GGGGACAGCTCTGGCTCTACCTTAGACCCCTGAACAAGAGGAGGAC 681
|||||
425 .....PheAlaLeuArgValLeu.....GluArgTh 433
682 ACATATACAAATGAGCAGGTACGGCAAGAGAGCAAAAGAATGTTCCCAAG 731
433 rGlyLeuGluAspPheGln..... 439
732 CTCTCAGCTGATCTTGACATGTATGATGGAAGCCAGTGAAGAAATGCA 781
440 .....AspIleLeuAsnGly 444
782 TTAGATTTAAAGTTTATATGAACAACCTGAAGACTCTATTGATAGGA 831
|||||
445 IleGlu.....GluPheLeuArgLeuGluProGlnAlaAspArgGl 458
832 AAAATACACAACTAATGGACATCTTTTGGTGGAGACACGGTTATTGAGA 881
|||||
458 uArgIleGlyIleThrGlyIleSerTyrGlyGlyTyrMetThrAsnTrpA 475

```

```

882 CTCCTAGTGAAGATCAGAGATTCAGATGTGTGATTATGCC..... 919
|||||
475 IaLeuThrGlnSerAspLeuPheLysAlaGlyIleSerGluAsnGlyIle 491
920 .....CTGGATGCATGCATGTTT..... 937
|||||
492 SerTyrTrpLeuThrSerTyrAlaPheSerAspIleGlyLeuTrpPheAs 508
938 .....CCACTGGGTGATGAATATATTCAGAA 965
|||||
508 pLysGluValIleGlyAspAsnProLeuGluAsnGluAsnTyrArgLysL 525
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966 TTCCTCAGCCCTCTTTT 985
525 eu.....SerProLeuPheTyr 530

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seq\_name: sp\_bacteria:087543

seq\_documentation\_block:

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ID 087543 PRELIMINARY; PRT; 237 AA.
AC 087543;
DT 01-NOV-1998 (TREMELREL. 08, Created)
DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)
DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN ADHESIN (FRAGMENT).
OS Capnocytophaga gingivialis.
OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DR2001;
RA Tempro P.J.;
RT "Capnocytophaga outer-membrane adhesin DNA sequence, 3'end.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083393; AAC35353.1; ..
DR MEROPS; S09.013; -.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR01375; Peptidase_S9.
DR InterPro; IPR002471; Prol_endopep_ser.
DR Pfam; PF00326; Peptidase_S9; 1.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
FT NON_TER
SQ SEQUENCE 237 AA; 27482 MW; 4D630AC81D64EDAC CRC64;

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alignment\_scores:

Quality:	108.50	Length:	240
Ratio:	0.986	Gaps:	9
Percent Similarity:	45.833	Percent Identity:	20.833

alignment\_block:

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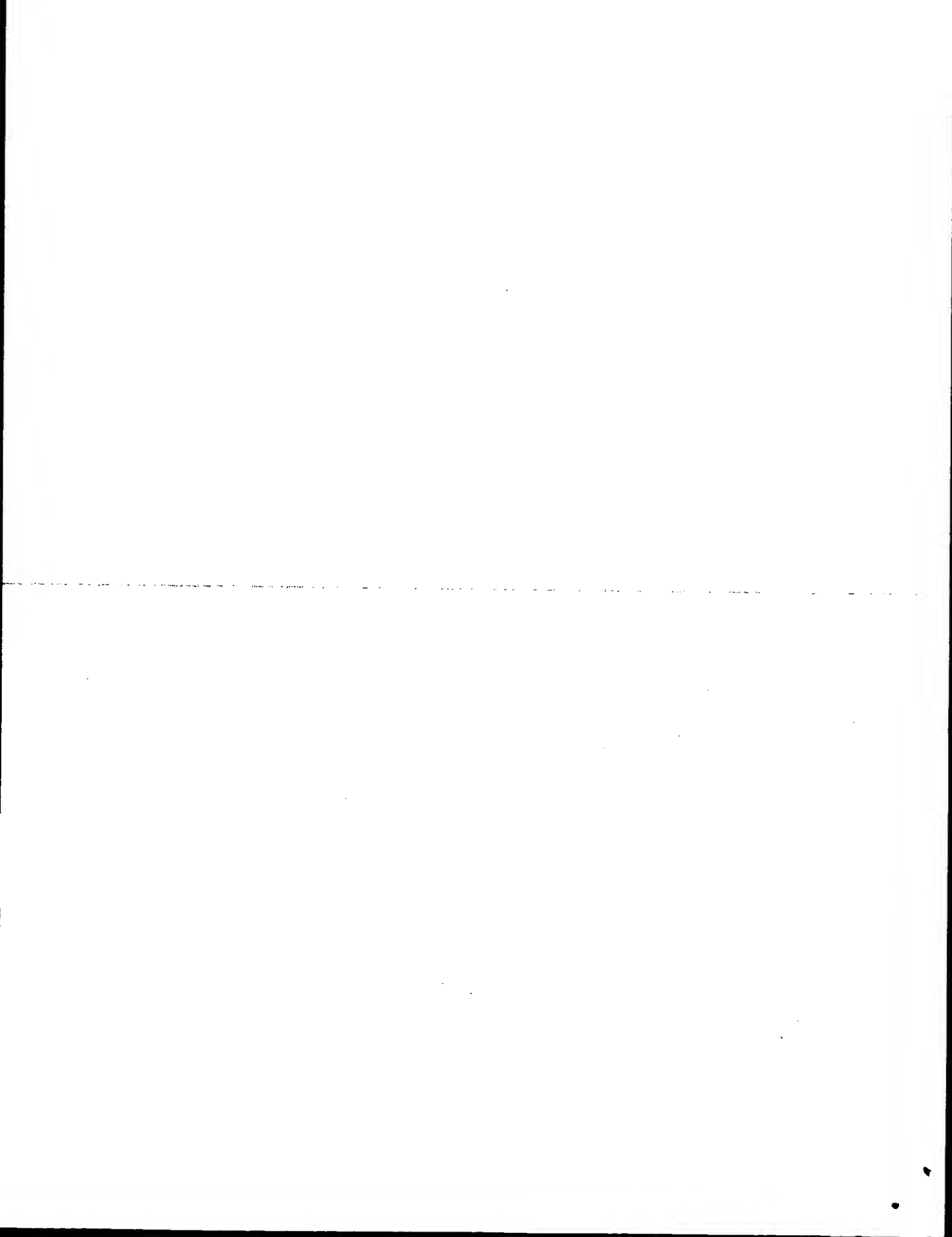
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419 ATCAACAACCTCTGCAACCTGGAATTCCTCTCAGGCCCTGTGCAAAATA 468
|||||
15 MeLileLysProSerAspPheAsnGlu.....AsnLysLysTy 27
469 TCACATGTGTGTTTTTCTCAT...GGTCTGGGCATTCAGACACATTT 515
|||||
27 rProLeuLeuMetPheGlnTyrSerGlyProGlySerGlnGlnValHisA 44
516 ATTCTGCTATTGGCATTGAC.....CTGGCATCTCAT 547
|||||
44 snSerPheSerGlyPheAspThrPheTrpTyrMetLeuAlaGlnLys 60
548 GGGTTTATAGTCTGCTGTAGAACACACAGATAGATCTGTCATCTGCAAC 597
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61 GlyTyrIleValLeuCysValAspGlyArgGlyThrGlyTyrLysGlyAl 77
598 TTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGC 647

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77 aaLaPhe...:::LySLysCyst 83
648 TCTACCTTTGAACCCCTGAAACAAGAGGAGACATATACCAATGAG 697
    ||| ::: ||| ||| ::::::::::
83 hrTyRLysGLnLeuGLyLysTyRGLuLeuGLuaSPGLnValGLuaLaAa 99
698 CAGGTACGGCAAGACCAAGAATGTTCCCAAGCTCTCAGTGTATTCT 747
    :::::: :|||
100 LysIleValcLYsnTyRLys..... 106
748 TGACATTGCATCGGAAGCCACTGAAGATGCATTAGATTAAAAGTTTG 797
    106 ..... 106
798 ATATGGAACAACGAGGACTCTATTTCATAGGAAAAAATACAGTAATT 847
    ||||||:||||:||||:||||:
107 .....TyRIeASpLYAspArgIleGLyILeITrp 116
848 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTTTCWAGTAGGATCA 897
    ||| |||||||||::: ::: :|||
117 GLYTrpSerPhcGLyGLYPHeMetAlaSerAsnCysILEtuARgGLyGL 133
898 GAGATTACAGATGGTRATGCC.....CTGGATGCATGCAGATGTTT. 937
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133 uMetPhLYsMetSerILEaValAlaProValThrAsnTrpArgPHeT 150
938 .....CCACTGGGTGATGAAGTATATTCAGAAATTCCTCAG.....CCC 976
    |||::: ||| ||| ||| |||
150 yrAspThrValTYthrGLUArGYrMetGLNThrPROGLnGLUAasnPro 166
977 CTCTTTTTTATCACTCTGAATATTTCCCATATCTCGTCVTAANTATCATAA 1025
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167 GLUClyTyRASpAsnAsnSerProLeUTHrTyRALysASNLeu..... 181
11027 AATGAAAAAATGCTACTCACCTCGATTAAGAACAAAGATGNTTACAAATCA 1076
    ::::::: |||::: |||
182 .....AsnLYSLysPHeLeuLeuValH 189
1077 GGGTTCAGTCCACCAGAAT 1096
    :|||::: |||
189 ISGLYThrAlaASPaspAsn 195
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 Seconds  
(without alignments)  
4.528 Million cell updates/sec

Title: US-09-922-067-10  
Perfect score: 37  
Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	10	21	N-terminus #1 of p
2	37	100.0	441	16	Human acetyl hydro
3	37	100.0	441	16	Human acetyl hydro
4	37	100.0	441	16	Human acetyl hydro
5	37	100.0	441	16	Human acetyl hydro
6	37	100.0	441	16	Human acetyl hydro
7	37	100.0	441	16	Human acetyl hydro
8	37	100.0	441	16	Human acetyl hydro
9	37	100.0	441	16	Human acetyl hydro
10	37	100.0	441	16	Human acetyl hydro
11	37	100.0	441	16	Human acetyl hydro

12	37	100.0	441	16	Human acetyl hydro
13	37	100.0	441	16	Human plasma plate
14	37	100.0	441	18	Human platelet-act
15	37	100.0	441	18	Human plasma plate
16	37	100.0	441	18	Platelet-activatin
17	37	100.0	441	19	Human plasma plate
18	37	100.0	441	20	Human plasma plate
19	37	100.0	441	20	Human PAF-AH prote
20	37	100.0	441	21	Plasma platelet-ac
21	37	100.0	441	21	Human low density
22	37	100.0	441	21	Human platelet-act
23	37	100.0	441	21	Human PAF-AH prote
24	37	100.0	441	22	Human plasma plate
25	37	100.0	441	22	Human plasma plate
26	37	100.0	441	22	Human plasma plate
27	37	100.0	441	22	Human plasma plate
28	37	100.0	441	22	Human plasma plate
29	37	100.0	441	22	Human plasma plate
30	37	100.0	441	22	Human plasma plate
31	37	100.0	441	22	Human plasma plate
32	37	100.0	441	22	Human plasma plate
33	37	100.0	441	22	Human platelet-act
34	37	100.0	441	22	Human plasma plate
35	37	100.0	441	22	Human plasma plate
36	37	100.0	441	22	Human plasma plate
37	37	100.0	441	22	Human plasma plate
38	37	100.0	441	22	Human plasma plate
39	37	100.0	441	22	Human plasma plate
40	37	100.0	441	22	Human plasma plate
41	32	86.5	155	21	Human T-cell lymph
42	32	86.5	285	21	Corn diacylglycerol
43	32	86.5	327	21	Corn diacylglycerol
44	32	86.5	361	21	Corn diacylglycerol
45	32	86.5	500	21	Rice diacylglycerol

ALIGNMENTS

RESULT 1  
AAB01944  
ID AAB01944 standard; peptide; 10 AA.  
XX  
AC AAB01944;  
XX  
DT 18-SEP-2000 (first entry)  
XX  
DE N-terminus #1 of purified recombinant human LDL-PLA2.

XX Human; low density lipoprotein associated phospholipase A2;  
KW LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;  
KW short chain phospholipid; serine-dependent phospholipase;  
KW inflammation; proinflammatory; anti inflammatory; drug screening;  
KW antibody; diagnosis; N-terminus.  
XX Homo sapiens.  
OS

XX Key Location/Qualifiers  
FH 1..10  
FT Region  
FT /note= "Corresponds to residues 22-31 of full-length  
human LDL-PLA2 (AAB01942)"  
XX

XX WO200024910-A1.  
XX  
XX 04-MAY-2000.  
XX  
XX 27-OCT-1999; 99WO-GB03551.  
XX  
XX 28-OCT-1998; 98GB-0023647.  
XX 28-OCT-1998; 98GB-0023648.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX

XX  
XXPT  
New nucleic acid encoding platelet activating factor,



PT acetyl:hydrolase - useful in diagnosis and for treating  
 XX inflammatory diseases, e.g. pleurisy  
 PS Example 10; : 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 DB 25 qyinpva 31  
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# RESULT 4

ID AAR73050 standard; Protein; 441 AA.

XX AAR73050;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C407S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX disease; pleurisy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 407

FT /note- "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

PS Example 10; : 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original

CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

QY 1 QYINPVA 7  
 DB 25 qyinpva 31  
 |||||

# RESULT 5

ID AAR71920 standard; Protein; 441 AA.

XX AAR71920;

XX 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant SI08A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX disease; pleurisy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108

FT /note- "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match

100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
| | | | |  
Db 25 qyinpva 31

## RESULT 6

AAR71921  
ID AAR71921 standard; Protein; 441 AA.

XX AC AAR71921;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant S273A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 273  
XX /note= "Wild-type Ser is substd. by Ala."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
XX Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
XX acetyl:hydrolase - useful in diagnosis and for treating  
XX inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
XX made with single amino acid changes for the purposes of identifying  
XX the active site of AH. The sequences of these mutants are not given  
XX in the patent specification; they have been derived from the original  
XX wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory  
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
XX gene may also be used in raising monoclonal antibodies specific for AH  
XX that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

## Query Match

Best Local Similarity 100.0%; Score 37; DB 16; Length 441;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
| | | | |  
Db 25 qyinpva 31

## RESULT 7

AAR71922

ID AAR71922 standard; Protein; 441 AA.

XX AC AAR71922;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D296A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 296  
XX /note= "Wild-type Asp is substd. by Ala."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
XX Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
XX acetyl:hydrolase - useful in diagnosis and for treating  
XX inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
XX made with single amino acid changes for the purposes of identifying  
XX the active site of AH. The sequences of these mutants are not given  
XX in the patent specification; they have been derived from the original  
XX wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory  
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
XX gene may also be used in raising monoclonal antibodies specific for AH  
XX that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

## Query Match

Best Local Similarity 100.0%; Score 37; DB 16; Length 441;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
| | | | |  
Db 25 qyinpva 31

## RESULT 8

AAR71923  
ID AAR71923 standard; Protein; 441 AA.

XX AC AAR71923;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D339A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX disease; pleurisy; diagnosis.

XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 338  
 FT /note= "Wild-type Asp is substd. by Ala."  
 XX  
 XX  
 PN W09509921-A.  
 XX  
 XX 13-APR-1995.  
 XX  
 XX 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 XX WPI; 1995-155262/20.  
 XX  
 XX New nucleic acid encoding platelet activating factor,  
 PT acetyl-hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 PT  
 XX  
 XX Example 10; : 88pp; English.  
 PS  
 XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
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 XX Sequence 441 AA;  
 SQ

Query Match 100.0%; Score 37; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 DB 25 qyinpva 31  
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RESULT 9  
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 ID AAR71924 standard; Protein; 441 AA.  
 XX  
 AC AAR71924;  
 XX  
 XX 06-DEC-1995 (first entry)  
 DT  
 XX Human acetyl hydrolase (AH) mutant H351A.  
 DE  
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX disease; pleurisy; diagnosis.  
 KW  
 KW Homo sapiens.  
 XX  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 351  
 FT /note= "Wild-type His is substd. by Ala."  
 XX  
 XX W09509921-A.  
 PN  
 XX 13-APR-1995.  
 PD

XX 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 XX WPI; 1995-155262/20.  
 DR  
 XX New nucleic acid encoding platelet activating factor,  
 PT acetyl-hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 PT  
 XX  
 XX Example 10; : 88pp; English.  
 PS  
 XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
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 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 XX Sequence 441 AA;  
 SQ

Query Match 100.0%; Score 37; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 DB 25 qyinpva 31  
 |||||

RESULT 10  
 AAR71925  
 ID AAR71925 standard; Protein; 441 AA.  
 XX  
 AC AAR71925;  
 XX  
 XX 06-DEC-1995 (first entry)  
 DT  
 XX Human acetyl hydrolase (AH) mutant H395A/H399A.  
 DE  
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 XX disease; pleurisy; diagnosis.  
 KW  
 KW Homo sapiens.  
 XX  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 395  
 FT /note= "Wild-type His is substd. by Ala."  
 FT 399  
 FT /note= "Wild-type His is substd. by Ala."  
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 XX W09509921-A.  
 PN  
 XX 13-APR-1995.  
 PD  
 XX 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI

PI Wilder CL;  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; ; 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYINPVA 7  
 |||||  
 Db 25 qyinpva 31

RESULT 11  
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 ID AAR73046 standard; Protein; 441 AA.  
 XX  
 AC AAR73046;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant C67S.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 67 /note= "Wild-type Cys is substd. by Ser."  
 FT  
 XX WO9509921-A.  
 XX 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; ; 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYINPVA 7  
 |||||  
 Db 25 qyinpva 31

RESULT 12  
 AAR73047  
 ID AAR73047 standard; Protein; 441 AA.  
 XX  
 AC AAR73047;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant C229S.  
 XX  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 229 /note= "Wild-type Cys is substd. by Ser."  
 FT  
 XX WO9509921-A.  
 XX 13-APR-1995.  
 XX  
 PF 06-OCT-1994; 94WO-US11340.  
 XX  
 PR 06-OCT-1993; 93US-0133803.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1995-155262/20.  
 XX  
 PT New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy  
 XX  
 PS Example 10; ; 88pp; English.  
 XX  
 CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).  
 CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;  
SQ

Query Match 100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPVA 7  
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|  
|  
|  
Db 25 qyinpva 31

RESULT 13

AAW71913  
ID AAR71913 standard; Protein; 441 AA.

XX  
AC AAR71913;

XX  
DT 05-DEC-1995 (first entry)

XX Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX disease; pleurisy; diagnosis.

OS Homo sapiens.

XX W09509921-A.

PN 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
XX Wilder CL;

XX WPI: 1995-155262/20.  
XX N-PSDB; AAQ87947.

XX New nucleic acid encoding platelet activating factor,  
XX acetyl hydrolase - useful in diagnosis and for treating  
XX inflammatory diseases, e.g. pleurisy

XX Claim 5; Page 53-54; 88pp; English.

XX The human acetyl hydrolase gene (AAQ87947) has been isolated and  
XX purified. The platelet activating factor acetyl hydrolase (AAR71913)  
XX is useful in the treatment of inflammatory diseases, in particular  
XX pleurisy, asthma, rhinitis and eczema. The gene may also be used in  
XX raising monoclonal antibodies specific for PAF-AH that are useful in  
XX the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPVA 7  
|  
|  
|  
|  
|  
|  
|  
Db 25 qyinpva 31

RESULT 14

AAW26498  
ID AAW26498 standard; Protein; 441 AA.

XX

AC AAW26498;

XX 05-JAN-1998 (first entry)

XX Human platelet-activating factor acetylhydrolase.

XX Platelet-activating factor acetylhydrolase; PAF-AH; human;  
XX inflammation; asthma; pleurisy; necrotising enterocolitis;  
XX adult respiratory distress syndrome; therapy.

OS Homo sapiens.

XX US5656431-A.

PN 12-AUG-1997.

XX 06-OCT-1993; 93US-0133803.

XX 07-JUN-1995; 95US-0483232.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
XX Wilder CL;

XX WPI: 1997-414580/38.  
XX N-PSDB; AAT87048.

XX Detecting lesions in human platelet-activating factor  
XX acetylhydrolase gene - by comparison with defined wild-type gene  
XX sequence

XX Example 3; Column 47-50; 53pp; English.

XX This polypeptide comprises human plasma platelet-activating factor  
XX acetylhydrolase (PAF-AH), a protein that inactivates PAF and  
XX inactivates oxidatively fragmented phospholipids such as products of  
XX the arachidonic acid cascade that mediate inflammation. Its  
XX sequence was deduced from a full-length cDNA clone (see AAT87048)  
XX obtained from a macrophage cDNA library. Mouse, dog, cattle,  
XX chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have  
XX also been identified. Recombinant PAF-AH polypeptides can be  
XX produced in prokaryotic or eukaryotic host cells and used to mimic  
XX or augment normal processes of resolution of inflammation in vivo.  
XX Examples describe the in vivo therapeutic effect of recombinant  
XX PAF-AH products on acute inflammation, pleurisy, asthma,  
XX necrotising enterocolitis and adult respiratory distress syndrome  
XX in animal models.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 18; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

Qy 1 QYINPVA 7  
|  
|  
|  
|  
|  
|  
|  
Db 25 qyinpva 31

RESULT 15

AAW23796  
ID AAW23796 standard; Protein; 441 AA.

XX AAW23796;

XX 04-NOV-1997 (first entry)

XX Human plasma platelet activating factor acetylhydrolase.

XX

KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;  
 KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;  
 KW central nervous system shock; arthritis; Crohn's disease;  
 XX systemic lupus erythematosus; adult respiratory distress syndrome.

XX Homo sapiens.

OS  
 XX US5641669-A.

XX  
 PN 24-JUN-1997.

XX  
 PD 06-OCT-1993; 93US-0133803.

XX  
 PF 06-OCT-1994; 94US-0318905.

XX  
 PR 06-OCT-1993; 93US-0133803.

XX  
 XX (ICOS-) ICOS CORP.

XX  
 PA Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;  
 PI Wilder CL;

XX  
 PI WPI; 1997-340947/31.

XX  
 DR N-PSDB; AAT80564.

XX  
 PT New human plasma platelet activating factor acetylhydrolase -

XX  
 PT useful as anti-inflammatory for treatment of asthma, anaphylaxis,  
 PT shock, etc

XX  
 PS Claim 1; Column 35-38; 43pp; English.

XX  
 CC The present sequence represents the purified and isolated human plasma

XX  
 CC platelet activating factor acetylhydrolase (PAF-AH). This novel

XX  
 CC polypeptide inactivates PAF and oxidatively fragmented phospholipids

XX  
 CC such as pro-inflammatory arachidonic acid metabolites, and so can be

XX  
 CC used to treat inflammation by augmenting endogenous activity. Typical

XX  
 CC applications are in asthma, anaphylaxis, shock, reperfusion injury,

XX  
 CC central nervous system shock, arthritis, Crohn's disease, systemic

XX  
 CC lupus erythematosus, adult respiratory distress syndrome. The

XX  
 CC polypeptide can also be used to raise specific antibodies (Ab) which

XX  
 CC are useful as immunoassay reagents and for generating anti-idiotypic

XX  
 CC antibodies. The nucleic acid encoding the protein can be used to screen

XX  
 CC for related genes; in hybridisation assays to assess the protein

XX  
 CC producing cells; to generate knockout mice; to detect genetic mutations

XX  
 CC and (antisense sequences) to inhibit the protein expression. Unlike PAF

XX  
 CC receptor antagonists, the protein is a natural component of plasma.

XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 18; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYINPVA 7  
 |  
 Db 25 qyinpva 31

Search completed: March 9, 2002, 00:31:57  
 Job time: 443 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:33:00 ; Search time 47.03 Seconds  
(without alignments)  
3.349 Million cell updates/sec

Title: US-09-922-067-10

Perfect score: 37

Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/pdata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/pdata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/pdata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/pdata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/pdata/2/1aa/6C\_COMB.pep:\*
- 6: /cgn2\_6/pdata/2/1aa/6D\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	7	2	US-08-557-892-10
2	37	100.0	7	2	US-08-387-858A-10
3	37	100.0	7	4	US-09-294-384B-10
4	37	100.0	441	1	US-08-470-187-8
5	37	100.0	441	1	US-08-318-905-8
6	37	100.0	441	1	US-08-483-232-8
7	37	100.0	441	1	US-08-483-140-8
8	37	100.0	441	2	US-08-485-938A-8
9	37	100.0	441	2	US-08-910-041-8
10	37	100.0	441	3	US-09-328-474-8
11	37	100.0	441	3	US-09-100-546-8
12	37	100.0	441	4	US-09-010-715-8
13	37	100.0	441	4	US-08-577-758-8
14	29	78.4	27	2	US-08-557-892-3
15	29	78.4	27	2	US-08-387-858A-3
16	29	78.4	27	4	US-09-294-384B-3
17	29	78.4	282	3	US-09-136-442-4
18	29	78.4	520	2	US-08-482-728A-4
19	29	78.4	520	4	US-09-028-366-5
20	28	75.7	272	1	US-08-252-995D-14
21	28	75.7	272	2	US-08-834-108-14
22	28	75.7	541	2	US-08-484-438-6
23	28	75.7	603	4	US-09-198-122-2
24	28	75.7	621	2	US-08-419-652-4
25	28	75.7	660	1	US-08-248-532-3
26	28	75.7	660	2	US-08-419-652-3
27	28	75.7	662	1	US-08-248-532-2

28 28 75.7 662 2 US-08-419-652-2 Sequence 2, Appli  
29 28 75.7 662 2 US-08-685-118-4 Sequence 4, Appli  
30 28 75.7 662 2 US-08-915-495-4 Sequence 4, Appli  
31 28 75.7 662 2 US-08-914-520-4 Sequence 2, Appli  
32 28 75.7 662 3 US-08-789-350-2 Sequence 4, Appli  
33 28 75.7 705 2 US-08-456-647B-4 Sequence 4, Appli  
34 28 75.7 705 2 US-08-237-401A-4 Sequence 7, Appli  
35 28 75.7 718 2 US-08-974-565C-7 Sequence 7, Appli  
36 28 75.7 718 2 US-09-255-748-7 Sequence 2, Appli  
37 28 75.7 1308 2 US-08-484-438-2 Sequence 32, Appli  
38 27 73.0 22 3 US-09-101-146-32 Sequence 7, Appli  
39 27 73.0 77 4 US-09-246-500B-7 Sequence 6, Appli  
40 27 73.0 257 3 US-09-101-146-6 Sequence 1, Appli  
41 27 73.0 345 3 US-09-101-146-1 Sequence 8, Appli  
42 27 73.0 477 3 US-08-843-982B-8 Sequence 1, Appli  
43 27 73.0 478 4 US-09-272-114-1 Sequence 2, Appli  
44 27 73.0 478 4 US-09-249-338-2 Sequence 4, Appli  
45 27 73.0 548 2 US-09-032-315-4

#### ALIGNMENTS

#### RESULT 1

US-08-557-892-10  
; Sequence 10, Application US/08557892  
; Patent No. 5968818  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Glover, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557,892  
; FILING DATE: 14 No. 5968818ember 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,858  
; FILING DATE: 14 No. 5968818ember 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dustman, Wayne J.  
; REGISTRATION NUMBER: 33,870  
; REFERENCE/DOCKET NUMBER: P30693C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5023  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; FRAGMENT TYPE: Internal  
US-08-557-892-10

Query Match 100.0%; Score 37; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 |||||  
 DB 1 QYINPVA 7

## RESULT 2

US-08-387-858A-10  
 ; Sequence 10, Application US/08387858A  
 ; Patent No. 5981252  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MacPhee, Colin Houston  
 ; APPLICANT: Tew, David Graham  
 ; APPLICANT: Southan, Christopher Donald  
 ; APPLICANT: Hickey, Dierdre Mary Bernadette  
 ; APPLICANT: Glover, Israel Simon  
 ; APPLICANT: Lawrence, Geoffrey Mark Prouse  
 ; APPLICANT: Rice, Simon Quentyn John  
 ; TITLE OF INVENTION: Compounds  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION NUMBER: US/08/387,858A  
 ; FILING DATE: 24 February 1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB94/01374  
 ; FILING DATE: 24 June 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dustman, Wayne J.  
 ; REGISTRATION NUMBER: 33,870  
 ; REFERENCE/DOCKET NUMBER: P30693  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5023  
 ; TELEFAX: 610-270-5090  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: internal  
 ; US-08-387-858A-10

Query Match 100.0%; Score 37; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 |||||  
 DB 1 QYINPVA 7

## RESULT 3

US-09-294-384B-10  
 ; Sequence 10, Application US/09294384B  
 ; Patent No. 6177257  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MacPhee, Colin Houston  
 ; APPLICANT: Tew, David Graham  
 ; APPLICANT: Southan, Christopher Donald  
 ; APPLICANT: Hickey, Dierdre Mary Bernadette  
 ; APPLICANT: Glover, Israel Simon  
 ; APPLICANT: Lawrence, Geoffrey Mark Prouse  
 ; APPLICANT: Rice, Simon Quentyn John  
 ; TITLE OF INVENTION: Compounds  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION NUMBER: US/09/294,384B  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/387,858  
 ; FILING DATE: 24 February 1995  
 ; APPLICATION NUMBER: PCT/GB94/01374  
 ; FILING DATE: 24 June 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dustman, Wayne J.  
 ; REGISTRATION NUMBER: 33,870  
 ; REFERENCE/DOCKET NUMBER: P30693  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5023  
 ; TELEFAX: 610-270-5090  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: internal  
 ; US-09-294-384B-10

Query Match 100.0%; Score 37; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 |||||  
 DB 1 QYINPVA 7

## RESULT 4

US-08-470-187-8  
 ; Sequence 8, Application US/08470187  
 ; Patent No. 5532152  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cousens, Lawrence S.  
 ; APPLICANT: Eberhardt, Christine E.  
 ; APPLICANT: Gray, Patrick W.  
 ; APPLICANT: Tjoelker, Larry W.  
 ; APPLICANT: Wilder, Cheryl L.  
 ; TITLE OF INVENTION: Platelet-Activating Factor Acetyl



TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,187  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5532152and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31672  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-470-187-8

Query Match 100.0%; Score 37; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYINPVA 7  
|||||  
Db 25 QYINPVA 31

RESULT 5  
US-08-318-905-8  
Sequence 8, Application US/08318905  
Patent No. 5641669  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,905  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5641669and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32205  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-905-8

Query Match 100.0%; Score 37; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYINPVA 7  
|||||  
Db 25 QYINPVA 31

RESULT 6  
US-08-483-232-8  
Sequence 8, Application US/08483232  
Patent No. 5656431  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,232  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5656431and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32689

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-232-8

Query Match 100.0%; Score 37; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
|||||  
DB 25 QYINPVA 31

RESULT 7  
US-08-483-140-8  
; Sequence 8, Application US/08483140  
; Patent No. 5698403  
; GENERAL INFORMATION:  
; APPLICANT: ICOS Corporation  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,140  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 6-OCT-1994  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-140-8

Query Match 100.0%; Score 37; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
|||||  
DB 25 QYINPVA 31

RESULT 8  
US-08-485-938A-8  
; Sequence 8, Application US/08485938A  
; Patent No. 5847088  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hal  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,938A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-485-938A-8

Query Match 100.0%; Score 37; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
|||||  
DB 25 QYINPVA 31

RESULT 9  
US-08-910-041-8  
; Sequence 8, Application US/08910041  
; Patent No. 5977308  
; GENERAL INFORMATION:

APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,041  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,232  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27866/34026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-910-041-8

Query Match 100.0%; Score 37; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
Db 25 QYINPVA 31

RESULT 10  
US-09-328-474-8  
Sequence 8, Application US/09328474  
Patent No. 6045794  
GENERAL INFORMATION:  
APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/328,474  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,232  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 27866/34026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-328-474-8

Query Match 100.0%; Score 37; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
Db 25 QYINPVA 31

RESULT 11  
US-09-100-546-8  
Sequence 8, Application US/09100546  
Patent No. 6099836  
GENERAL INFORMATION:  
APPLICANT: Cousins, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
TITLE OF INVENTION: Acetylhydrolase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,546  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6099836and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: proteln  
US-09-100-546-8

Query Match 100.0%; Score 37; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
DB 25 QYINPVA 31

RESULT 12  
US-09-010-715-8  
Sequence 8, Application US/09010715  
Patent No. 614625  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,715  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,905  
FILING DATE: 06-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6146625and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-010-715-8

Query Match 100.0%; Score 37; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
DB 25 QYINPVA 31

RESULT 13  
US-09-577-758-8  
Sequence 8, Application US/09577758  
Patent No. 6203790  
GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/577,758  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/010,715  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 06-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6203790and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/32793  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-577-758-8

Query Match 100.0%; Score 37; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPVA 7  
Db 25 QYINPVA 31

RESULT 14

US-08-557-892-3  
; Sequence 3, Application US/08557892  
; Patent No. 5968018  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Glover, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557,892  
; FILING DATE: 14 No. 5968818ember 1995  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-557-892-3

Query Match 78.4%; Score 29; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINP 5  
Db 1 QYINP 5

RESULT 15

US-08-387-858A-3  
; Sequence 3, Application US/08387858A  
; Patent No. 5981252  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Glover, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,858A  
; FILING DATE: 24 February 1995  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-387-858A-3

Query Match 78.4%; Score 29; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINP 5  
Db 1 QYINP 5

Search completed: March 9, 2002, 00:33:01  
Job time: 402 sec

Mon Mar 11 10:01:48 2002

us-09-922-067-10.rai

Page 8

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:11 ; Search time 53.53 Seconds  
(without alignments)  
9.961 Million cell updates/sec

Title: US-09-922-067-10

Perfect score: 37

Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.68.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	441	2 S60247	platelet-activating
2	32	86.5	231	2 T01294	sterol O-acyltrans
3	32	86.5	441	2 H84576	diacylglycerol O-a
4	32	86.5	520	2 T52584	diacylglycerol O-a
5	32	86.5	605	2 S52253	copper resistance
6	32	86.5	716	1 WZBEE6	77.8K DNA helicase
7	32	86.5	723	1 RRWOTN	RNA-directed RNA p
8	31	83.8	764	2 T39878	hypothetical prote
9	31	83.8	771	2 F70701	probable biofz pro
10	31	83.8	1417	2 H83132	probable sensor/re
11	30	81.1	149	2 S75155	hypothetical prote
12	30	81.1	248	2 S34995	surface lipoprotei
13	30	81.1	283	2 S65961	mann protein - Par
14	30	81.1	420	2 T32426	hypothetical prote
15	30	81.1	454	2 S58148	hypothetical prote
16	30	81.1	698	2 C82332	translation elonga
17	30	81.1	753	2 S35371	finger protein neu
18	29	78.4	154	2 T14727	dehydrin DHN1 - so
19	29	78.4	235	2 T32462	hypothetical prote
20	29	78.4	295	2 B86320	3-phosphoserine ph
21	29	78.4	295	2 T51362	phosphoserine phos
22	29	78.4	353	2 S34347	GTP-binding regula
23	29	78.4	411	2 B69450	anthranilate synth
24	29	78.4	414	2 A24872	hypothetical prote
25	29	78.4	421	2 C82253	folypolylglutamate
26	29	78.4	444	2 T38760	hypothetical prote
27	29	78.4	462	2 H69751	amino acid permeas
28	29	78.4	520	1 S64705	cyclophilin-like p
29	29	78.4	524	2 T06021	hypothetical prote

30 29 78.4 525 1 S39834 myb-related protei  
31 29 78.4 700 2 T23629 hypothetical prote  
32 29 78.4 751 2 T42597 DNA helicase/prima  
33 29 78.4 757 2 J50198 genome polyprotein  
34 29 78.4 1208 2 T05077 hypothetical prote  
35 29 78.4 1407 1 BWBYM1 TATA box-binding p  
36 29 78.4 1409 2 S74916 alkaline phosphata  
37 29 78.4 1511 2 A53151 pleiotropic drug r  
38 29 78.4 1529 2 S69688 hypothetical prote  
39 29 78.4 2032 2 T39817 hypothetical prote  
40 29 78.4 2219 2 T27684 hypothetical prote  
41 29 78.4 4919 2 T31105 Ig kappa chain h  
42 28 75.7 124 2 S40364 hypothetical 15.7K  
43 28 75.7 143 2 JQ0446 yafM protein - Esc  
44 28 75.7 165 2 E64747 hypothetical prote  
45 28 75.7 210 2 T29346

## ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TIO>

A:Cross-references: EMBL:U20157; NID:G780132; PIDN:AA050126.1; PID:G780133

Query Match 100.0%; Score 37; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

Db 25 QYINPVA 31

RESULT 2

T01294

sterol O-acyltransferase homolog F27F23.26 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 30-Apr-1999

C:Accession: T01294

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;

submitted to the EMBL Data Library, May 1998

A:Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.

A:Reference number: Z14177

A:Accession: T01294

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-231 <ROD>

A:Cross-references: EMBL:AC003058; NID:G3135250; PID:G3135276

A:Experimental source: Cultivar Columbia

C:Genetics:

A:Map position: 2

A:Introns: 44/3; 70/3; 104/3; 150/2; 177/3; 184/3; 205/3

A>Note: F27F23.26

Query Match

Best Local Similarity 86.5%; Score 32; DB 2; Length 231;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
|||||  
Db 104 QYINPI 109

## RESULT 3

H84576  
diacylglycerol O-acyltransferase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: H84576  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: H84576  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-441 <STO>  
A:Cross-references: GB:AE002093; NID:94191775; PIDN:AAD10144.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g19450  
A:Map position: 2

Query Match 86.5%; Score 32; DB 2; Length 441;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
|||||  
Db 269 QYINPI 274

## RESULT 4

T52584  
diacylglycerol O-acyltransferase (EC 2.3.1.20) [validated] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 17-Nov-2000  
C:Accession: T52584  
R:Hills, M.J.; Lu, C.; Hobbs, D.H.  
PDBS Lett. 452, 145-149, 1999  
A:Title: Cloning of a cDNA encoding diacylglycerol acyltransferase from Arabidopsis thaliana.  
A:Reference number: Z26127  
A:Accession: T52584  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-520 <HIL>  
A:Cross-references: EMBL:AJ131831; PIDN:CAB44774.1  
A:Experimental source: cultivar Columbia  
C:Function:  
A:Description: EC 2.3.1.20 [validated; MUID:99313150]; catalyzes the final acylation of  
A:Pathway: triacylglycerol biosynthesis  
C:Keywords: acyltransferase; coenzyme A

Query Match 86.5%; Score 32; DB 2; Length 520;  
Best Local Similarity 83.3%; Pred. No. 34;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
|||||  
Db 331 QYINPI 336

## RESULT 5

S52253  
copper resistance protein pcoA precursor - Escherichia coli plasmid pRJ1004  
N:Alternate names: copper-binding protein  
C:Species: Escherichia coli

C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 11-Jun-1999  
C:Accession: S70159; S52253  
R:Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.  
Mol. Microbiol. 17, 1153-1166, 1995  
A:Title: Molecular genetics and transport analysis of the copper-resistance deter  
A:Reference number: S70159; MUID:96130847  
A:Accession: S70159  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-605 <BRO>  
A:Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58525.1; PID:g619128  
C:Genetics:  
A:Gene: pcoA  
A:Genome: plasmid pRJ1004  
C:Superfamily: laccase  
C:Keywords: copper binding  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-605/Product: copper resistance protein pcoA #status predicted <MAT>

Query Match 86.5%; Score 32; DB 2; Length 605;  
Best Local Similarity 83.3%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
|||||  
Db 299 QYINPV 304

## RESULT 6

W2RE6  
77.8K DNA helicase/primase-associated protein - equine herpesvirus 1 (strain Ab4p)  
C:Species: equine herpesvirus 1  
A:Date: host Equus caballus (domestic horse)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 16-Jul-1999  
C:Accession: I36800  
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
submitted to GenBank, March 1992  
A:Description: The DNA sequence of equine herpesvirus-1.  
A:Reference number: A36805  
A:Accession: I36800  
A:Molecule type: DNA  
A:Residues: 1-716 <TEL>  
A:Cross-references: GB:M86664; NID:g330791; PIDN:AAB02489.1; PID:g330845  
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
Virology 189, 304-316, 1992  
A:Title: The DNA sequence of equine herpesvirus-1.  
A:Reference number: A41831; MUID:92295566  
A:Contents: annotation; possible protein-coding frames  
A:Note: neither amino acid nor nucleotide sequence is given  
C:Genetics:  
A:Gene: 54  
C:Superfamily: varicella-zoster virus gene 52 protein

Query Match 86.5%; Score 32; DB 1; Length 716;  
Best Local Similarity 85.7%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
|||||  
Db 430 QHINPVA 436

## RESULT 7

RRWOTN  
RNA-directed RNA polymerase (EC 2.7.7.48) - tobacco necrosis virus (strain A)  
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase  
N:Contents: 23K protein  
C:Species: tobacco necrosis virus, TNV  
A:Note: host Phaseolus vulgaris (kidney bean)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 11-Jun-1999  
C:Accession: A35523



R:Meulewaeter, F.; Seurinck, J.; van Emmelo, J.  
 Virology 177, 699-709, 1990  
 A:Title: Genome structure of tobacco necrosis virus strain A.  
 A:Reference number: A35523; MUID:90320143  
 A:Accession: A35523  
 A:Molecule type: genomic RNA  
 A:Residues: 1-723 <MEUS>  
 A:Cross-references: EMBL:M33002; NID:gl172549; PIDN:AAA86434.1; PID:g310915  
 A:Note: readthrough of the terminator UAG occurs between codons AAA for 202-Lys and GGG  
 C:Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwarf  
 C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication  
 F:1-202/Product: 23k protein #status predicted <KPP>  
 F:427-593/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD>

Query Match 86.5%; Score 32; DB 1; Length 723;  
 Best Local Similarity 71.4%; Pred. No. 49;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 :|||||  
 Db 419 KYNPVA 425

RESULT 8  
 T39878  
 hypothetical protein SPBC20F10.07 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T39878  
 R:Lyne, M.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.  
 Submitted to the EMBL Data Library, February 1998  
 A:Reference number: 221888  
 A:Accession: T39878  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-764 <LYN>  
 A:Cross-references: EMBL:AL021747; PIDN:CAA16847.1; GSPDB:GN00067; SPDB:SPBC20F10.07  
 A:Experimental source: strain 972h; cosmid c20F10  
 C:Genetics:  
 A:Gene: SPDB:SPBC20F10.07  
 A:Map position: 2

Query Match 83.8%; Score 31; DB 2; Length 764;  
 Best Local Similarity 85.7%; Pred. No. 87;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 :|||||  
 Db 489 QYIRPVA 495

RESULT 9  
 F70701  
 probable bioF2 protein - Mycobacterium tuberculosis (strain H37Rv)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 18-Feb-2000  
 C:Accession: F70701  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;  
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987  
 A:Accession: F70701  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-771 <COL>  
 A:Cross-references: GB:280233; GB:AL123456; NID:g3261645; PIDN:CAH02417.1; PID:ez66944;  
 A:Experimental source: strain H37Rv  
 C:Genetics:

A:Gene: bioF2  
 C:Superfamily: glycine C-acetyltransferase homology  
 C:Keywords: phosphoprotein; pyridoxal phosphate  
 F:615/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 83.8%; Score 31; DB 2; Length 771;  
 Best Local Similarity 83.3%; Pred. No. 87;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7  
 :|||||  
 Db 721 YVNPVA 726

RESULT 10  
 HB3132  
 probable sensor/response regulator hybrid PA4112 [imported] - Pseudomonas aeruginosa  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: HB3132  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrner, P.; Hickey, M.J.;  
 Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;  
 Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A:Reference number: A82950; MUID:20437337  
 A:Accession: HB3132  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1417 <STO>  
 A:Cross-references: GB:AE004827; GB:AE004091; NID:g9950306; PIDN:AAG07499.1; GSPDB:G  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA4112

Query Match 83.8%; Score 31; DB 2; Length 1417;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 :|||||  
 Db 147 QYIEPVA 153

RESULT 11  
 S75155  
 hypothetical protein sll1638 - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 C:Accession: S75155  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, J.;  
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yano, K.

DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
 A:Reference number: S74322; MUID:97061201  
 A:Accession: S75155  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-149 <KAN>  
 A:Cross-references: EMBL:D90903; GB:AB001339; NID:gl652127; PIDN:BAAL7069.1; PID:d10  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 81.1%; Score 30; DB 2; Length 149;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7  
 :|||||

Db 44 YVNPJA 49

## RESULT 12

S34995

surface lipoprotein p27 - Lyme disease spirochete (strain B29)

N:Alternate names: 27K antigen

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

A:Variety: strain B29

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999

C:Accession: S34995; S27487

R:Reindl, M.; Redl, B.; Stoeffler, G.

Mol. Microbiol. 8, 1115-1124, 1993

A:Title: Isolation and analysis of a linear plasmid-located gene of Borrelia burgdorferi

A:Reference number: S34995; MUID:93368427

C:Accession: S34995

A:Molecule type: DNA

A:Residues: 1-248 &lt;RET&gt;

A:Cross-references: EMBL:M85216; NID:g469167; PIDN:AAAL17494.1; PID:gl44008

A:Experimental source: Borrelia burgdorferi B29

C:Keywords: surface antigen

Query Match

Best Local Similarity 81.1%; Score 30; DB 2; Length 248;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6

|||:|:

Db 197 QYLNPI 202

## RESULT 13

S65961

mauN protein - Paracoccus denitrificans

C:Species: Paracoccus denitrificans

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 29-Sep-1999

C:Accession: S65961

R:van der Pahlen, C.J.N.M.; Slotboom, D.J.; Jongejan, L.; Reijnders, W.N.M.; Harms, N.;

Eur. J. Biochem. 230, 860-871, 1995

A:Title: Mutational analysis of mau genes involved in methylamine metabolism in Paracoccus

A:Reference number: S65958; MUID:95324575

C:Accession: S65961

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 &lt;VAN&gt;

A:Cross-references: EMBL:U15028; NID:g595839; PIDN:AAA86469.1; PID:g595843

C:Genetics:

A:Gene: mauN

C:Superfamily: hypothetical protein H10346; ferredoxin 2[4Fe-4S] homology

F:220-280/Domain: ferredoxin 2[4Fe-4S] homology &lt;PER&gt;

Query Match

Best Local Similarity 81.1%; Score 30; DB 2; Length 283;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

:|:|:|:

Db 159 EYVNPVS 165

## RESULT 14

T32426

hypothetical protein C10E2.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T32426

R:Wohlmann, P.; Sansone, J.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid C10E2.

A:Reference number: Z21165

A:Accession: T32426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-420 &lt;WOH&gt;

A:Cross-references: EMBL:AF026202; PIDN:AAH71242.1; GSPDB:GN00028; CESP:C10E2.2

A:Experimental source: strain Bristol N2; clone C10E2

C:Genetics:

A:Gene: CESP:C10E2.2

A:Map position: X

A:Introns: 5/2; 80/3; 160/3; 191/2; 245/2; 302/2; 335/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C10E2.2

Query Match

Best Local Similarity 81.1%; Score 30; DB 2; Length 420;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7

|||:|:

Db 364 QYFNPS 370

## RESULT 15

S58148

hypothetical protein SPAC2F7.04 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 04-Mar-2000

C:Accession: T38552; S58148

R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z21799

A:Accession: T38552

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-454 &lt;GE2&gt;

A:Cross-references: EMBL:Z50142; NID:gl052783; PIDN:CAA90491.1; PID:gl052787; GSPDB:

A:Experimental source: strain 972h-; cosmid c2F7

C:Genetics:

A:Gene: SPAC2F7.04

A:Map position: 1

A:Introns: 78/3; 294/3

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC2F7.04

Query Match

Best Local Similarity 81.1%; Score 30; DB 2; Length 454;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7

|||:|:

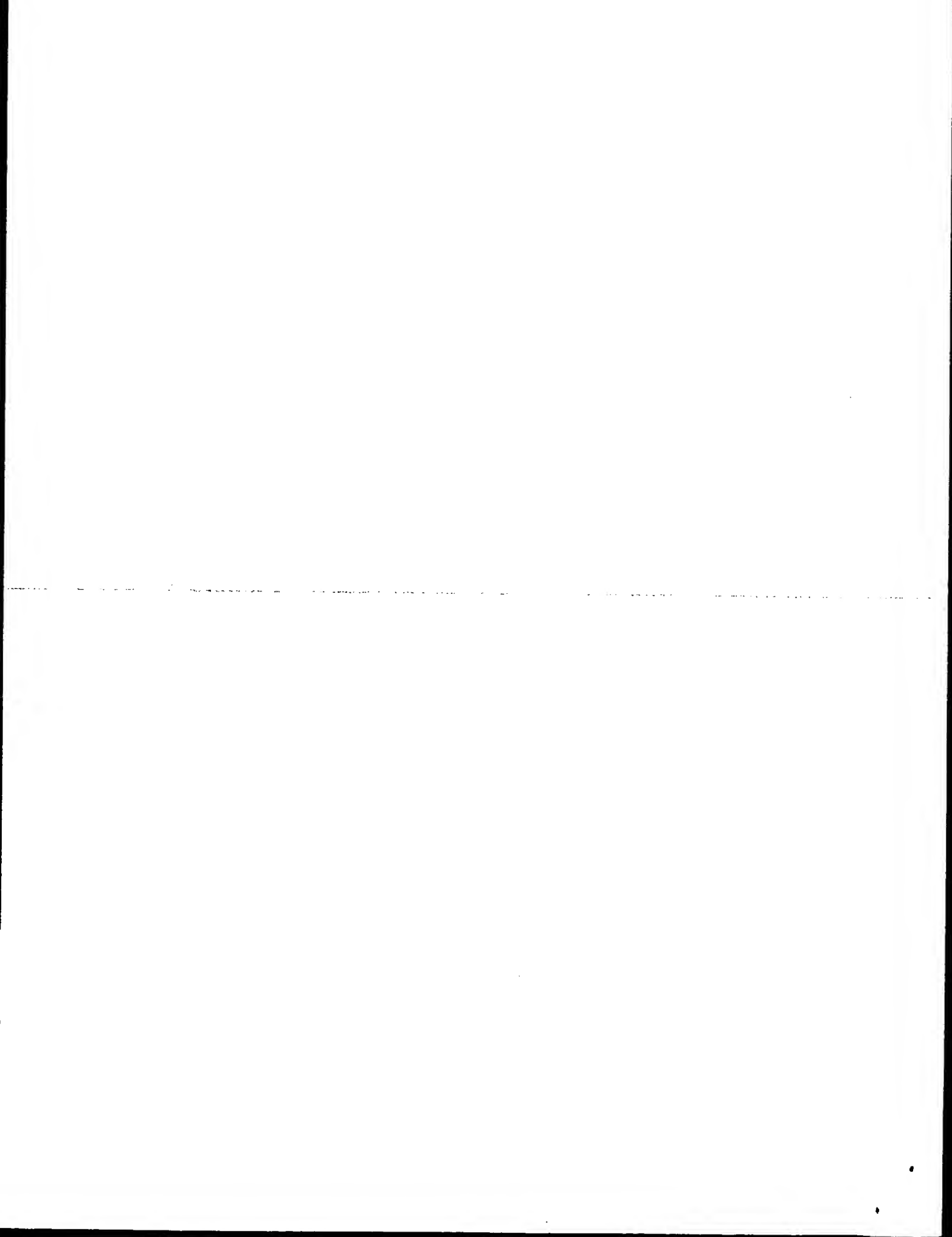
Db 103 QYNNPVA 109

Search completed: March 9, 2002, 00:34:13

Job time: 324 sec

Mon Mar 11 10:01:50 2002

us-09-922-067-10.rpr



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:36 ; Search time 30.16 Seconds  
(without alignments)  
8.510 Million cell updates/sec

Title: US-09-922-067-10

Perfect score: 37

Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	100.0	441	1 PAPA_HUMAN	Q13093 h platelet-
2	32	86.5	605	1 PCOA_ECOLI	Q47452 escherichia
3	32	86.5	716	1 HERA_HSVB	P28946 equine herp
4	32	86.5	723	1 RRPO_TNVA	P22958 tobacco nec
5	30	81.1	283	1 MAUN_PARDE	Q51660 paracoccus
6	30	81.1	454	1 YA24_SCHPO	Q09696 schizosacch
7	29	78.4	265	1 RUZA_DROME	Q9V498 drosophila
8	29	78.4	353	1 GBO_LYMS	P38411 lymnaea sta
9	29	78.4	411	1 TRPE_ARCFU	Q28669 archaeglob
10	29	78.4	414	1 YAG2_DROME	P20828 drosophila
11	29	78.4	444	1 YAG2_SCHPO	O10138 schizosacch
12	29	78.4	462	1 YBAG_BACSU	P54425 bacillus su
13	29	78.4	525	1 YBFA_YEAST	P34219 saccharomyc
14	29	78.4	791	1 TEX_BORPE	Q45388 bordetella
15	29	78.4	1407	1 T2D2_YEAST	P23255 saccharomyc
16	29	78.4	1499	1 CDR2_CANAL	P78595 candida alb
17	29	78.4	1511	1 PDR5_YEAST	P33302 saccharomyc
18	29	78.4	1529	1 PDRE_YEAST	O04182 saccharomyc
19	29	78.4	4823	1 YDRA_HUMAN	Q9N099 homo sapien
20	28	75.7	143	1 YDRA_HRORU	P14301 rhodospiril
21	28	75.7	165	1 YAFM_ECOLI	Q47152 escherichia
22	28	75.7	222	1 ERBA_RAT	Q62956 rattus norv
23	28	75.7	287	1 NAPH_HAEIN	P44630 haemophilus
24	28	75.7	344	1 VGLM_HSV62	Q04630 human herpe
25	28	75.7	346	1 OPLP_ICTPU	P52449 human herpe
26	28	75.7	346	1 AGAL_ECOLI	Q02266 ictalurus p
27	28	75.7	451	1 AGAL_ECOLI	P06720 escherichia
28	28	75.7	503	1 C303_DROME	Q9V399 drosophila
29	28	75.7	503	1 NQRE_CHLMU	O9K6b6 chlamydia m
30	28	75.7	575	1 PTL_HAEIN	P43922 haemophilus
31	28	75.7	603	1 PLK1_HUMAN	P53350 homo sapien
32	28	75.7	603	1 PLK1_MOUSE	Q07832 mus musculu
33	28	75.7	603	1 PLK1_RAT	Q62673 rattus norv

#### RESULT 1

ID	PAPA_HUMAN	STANDARD;	PRT;	441 AA.
AC	Q13093; Q15692;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)			
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED			
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE			
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).			
GN	PLAZG7 OR PAFAH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.			
RC	TISSUE=Myeloid;			
RX	MEDLINE=95214779; PubMed=7700381;			
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,			
RA	Schmelker B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,			
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;			
RT	*Anti-inflammatory properties of a platelet-activating factor			
RT	acetylhydrolase.*;			
RL	Nature 374:549-553(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Lymphoma;			
RX	MEDLINE=96197208; PubMed=8624782;			
RA	Tew D.G., Southern C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,			
RA	Moore K., Gloger I.S., Macphie C.H.;			
RT	*Purification, properties, sequencing, and cloning of a lipoprotein-			
RT	associated, serine-dependent phospholipase involved in the oxidative			
RT	modification of low-density lipoproteins.*;			
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).			
RN	[3]			
RP	MUTAGENESIS.			
RX	MEDLINE=96029630; PubMed=7592717;			
RA	Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,			
RA	Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,			
RT	*Plasma platelet-activating factor acetylhydrolase is a secreted			
RT	phospholipase A2 with a catalytic triad.*;			
RL	J. Biol. Chem. 270:25481-25487(1995).			
RN	[4]			
RP	VARIANT PHE-279.			
RX	MEDLINE=96359525; PubMed=8675689;			
RA	Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,			
RA	Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,			
RA	McIntyre T.M., Gray P.W., Prescott S.M.;			
RT	*Platelet-activating factor acetylhydrolase deficiency. A missense			
RT	mutation near the active site of an anti-inflammatory			
RT	phospholipase.*;			
RL	J. Clin. Invest. 97:2784-2791(1996).			
RN	[5]			

34	28	75.7	609	1 COPA_PSESM	P12374 pseudomonas
35	28	75.7	659	1 CN8E_HUMAN	O95263 homo sapien
36	28	75.7	662	1 IL2R_HUMAN	P42701 homo sapien
37	28	75.7	726	1 NU84_YEAST	P54891 saccharomyc
38	28	75.7	804	1 SYFB_BACSU	P17922 bacillus su
39	28	75.7	872	1 GUXA_CELFI	P50401 cellulomona
40	28	75.7	1227	1 LAF4_HUMAN	P51826 homo sapien
41	28	75.7	1308	1 ERB4_HUMAN	Q15303 homo sapien
42	28	75.7	1501	1 CDRL_CANAL	P43071 candida alb
43	28	75.7	1829	1 Y296_HUMAN	O15015 homo sapien
44	28	75.7	1849	1 BIG1_BOVIN	O46382 bos taurus
45	28	75.7	1849	1 BIG1_HUMAN	Q9Y6d6 homo sapien

#### ALIGNMENTS

RP VARIANT PHE-279.  
 RX MEDLINE=98430412; PubMed=9759612;  
 RA Yoshida H., Inaizumi T., Fujimoto K., Itaya H., Hiramoto M.,  
 RA Yoshimizu N., Fukushi K., Sato K.;  
 RT "A mutation in plasma platelet-activating factor acetylhydrolase  
 (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not  
 RT for hypertension.";  
 RL Thromb. Haemost. 80:372-375(1998).  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS  
 CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT  
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY  
 CC RESPONSES.  
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC -----  
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 CC -----  
 DR EMBL; U20157; AAC50126.1; -;  
 DR EMBL; U24577; AAB04170.1; -;  
 DR MIM; 601690; -;  
 DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro; IPR000734; Lipase.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 441  
 FT ACT\_SITE 273 273 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 296 296 ACETYLHYDROLASE.  
 FT ACT\_SITE 351 351 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 423 423 CHARGE RELAY SYSTEM.  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE  
 FT PROTEIN).  
 FT FTID=VAR\_004268.  
 FT MUTAGEN 108 108 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 FT MUTAGEN 273 273 S->A: LOSS OF ACTIVITY.  
 FT MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.  
 FT MUTAGEN 286 286 D->N: DIMINISHED ACTIVITY.  
 FT MUTAGEN 296 296 D->A: LOSS OF ACTIVITY.  
 FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.  
 FT MUTAGEN 304 304 D->A: NO CHANGE IN ACTIVITY.  
 FT MUTAGEN 338 338 H->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 FT MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.  
 FT CONFLICT 379 379 V -> A (IN REF. 2).  
 SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

Query Match 100.0%; Score 37; DB 1; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 Db 25 QYINPVA 31

RESULT 2

PCOA\_ECOLI  
 ID PCOA\_ECOLI STANDARD; PRT; 605 AA.  
 AC Q47452;  
 DT 20-AUG-2001 (Rel. 40, Last Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE COPPER RESISTANCE PROTEIN A PRECURSOR.  
 GN PCOA.  
 OS Escherichia coli.  
 OG Plasmid pRJ1004.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / ED8739;  
 RX MEDLINE=96130847; PubMed=8594334;  
 RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T.O., Rouch D.A.;  
 RT "Molecular genetics and transport analysis of the copper-resistance  
 RT determinant (pco) from Escherichia coli plasmid pRJ1004.";  
 RL Mol. Microbiol. 17:1153-1166(1995).  
 CC -!- FUNCTION: REQUIRED FOR THE COPPER-INDUCIBLE EXPRESSION OF COPPER  
 CC RESISTANCE. MAY HAVE OXIDASE ACTIVITY (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. COPA  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X83541; CAA58525.1; -;  
 DR InterPro; IPR001117; Cu-oxidase.  
 DR InterPro; IPR002355; Multicu\_Oxidase2.  
 DR Pfam; PF00394; Cu-oxidase; 2.  
 DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
 DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; 1.  
 KW Oxidoreductase; Copper; Repeat; Signal; Plasmid; Metal-binding;  
 KW Periplasmic.  
 FT SIGNAL 1 40 POTENTIAL.  
 FT CHAIN 41 605 COPPER RESISTANCE PROTEIN A.  
 FT DOMAIN 382 429 3 X 8 AA TANDEM REPEATS OF D-H-X-X-M-X-  
 FT G-M.  
 FT REPEAT 382 389 1.  
 FT REPEAT 414 421 2.  
 FT REPEAT 422 429 3.  
 FT METAL 100 100 COPPER (TYPE 2) (BY SIMILARITY).  
 FT METAL 102 102 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 142 142 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 144 144 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 538 538 COPPER (TYPE 1) (POTENTIAL).  
 FT METAL 541 541 COPPER (TYPE 2) (POTENTIAL).  
 FT METAL 543 543 COPPER (TYPE 3) (POTENTIAL).  
 FT METAL 586 586 COPPER (TYPE 3) (POTENTIAL).  
 FT METAL 587 587 COPPER (TYPE 1) (POTENTIAL).  
 FT METAL 588 588 COPPER (TYPE 3) (POTENTIAL).  
 FT METAL 592 592 COPPER (TYPE 1) (POTENTIAL).  
 FT METAL 597 597 COPPER (TYPE 1) (POTENTIAL).  
 SQ SEQUENCE 605 AA; 67307 MW; 8EECA1B2D56B27D8 CRC64;

Query Match 86.5%; Score 32; DB 1; Length 605;  
 Best Local Similarity 83.3%; Pred. No. 24;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
 Db 299 QYINPV 304

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CC EMBL; M33002; AAA86434.1; -;  
CC PIR; A35523; RRMQTN.  
DR InterPro; IPR002564; PV\_RDRP.  
DR Pfam; PF01615; PV\_RDRP; 1.  
KW Transferase; RNA-directed RNA polymerase.  
FT CHAIN 1 202 23 KDA PROTEIN.  
FT VARIANT 72 72 V -> A.  
FT VARIANT 698 698 K -> R.  
SQ SEQUENCE 723 AA; 82167 MW; DA9D142F0A3DE6D CRC64;

Query Match 86.5%; Score 32; DB 1; Length 723;  
Best Local Similarity 71.4%; Pred. No. 29;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
DB 419 KYNPVA 425  
:|||||

## RESULT 5

ID MAUN\_PARDE STANDARD; PRT; 283 AA.

AC Q51660; 1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE METHYLAMINE UTILIZATION FERREDOXIN-TYPE PROTEIN MAUN.  
GN MAUN.

OS Paracoccus denitrificans.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
OC PARACOCUS.  
OX NCBI\_TaxID=266;

## SEQUENCE FROM N.A.

RC STRAIN=PD 1222;  
RC MEDLINE=95324575; PubMed=7601147;  
RA van der Palen C.J., Slotboom D.J., Jongejan L., Reijnders W.N.,  
Harms N., Duine J.A., van Spanning R.J.;  
RT "Mutational analysis of man genes involved in methylamine metabolism  
in Paracoccus denitrificans."  
RT Eur. J. Biochem. 230:860-871(1995).

CC -I- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).

CC -I- PATHWAY: METHYLAMINE UTILIZATION.

CC -I- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF  
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.

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CC EMBL; U15028; AAA86469.1; -;  
CC HSSP; P00195; 1CLF.  
CC InterPro; IPR001450; 4FE4S\_ferredxin.  
DR Pfam; PF00037; fer4; 2.  
DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 2.  
KW Electron transport; Iron-sulfur; 4Fe-4S.

FT METAL 227 227 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 230 230 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 233 233 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 237 237 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 260 260 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 263 263 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 266 266 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 270 270 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

SQ SEQUENCE 283 AA; 31035 MW; FB2C87C9B8917EDE CRC64;

## RESULT 3

ID HEPA\_HSVB STANDARD; PRT; 716 AA.

AC P28946;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE DNA HELICASE/PRIMASE COMPLEX ASSOCIATED PROTEIN.

GN 54.

OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

OX NCBI\_TaxID=31520;

RT [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=92295566; PubMed=1318606;

RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;

RT "The DNA sequence of equine herpesvirus-1";

RL Virology 189:304-316(1992).

CC -I- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION.

CC -I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL8,

CC EHV-1 54, VZV 52 AND HCMV 102.

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CC EMBL; M86664; AAB02489.1; -;  
CC PIR; I36800; WZBEE6.  
CC DNA replication.

QY 1 QYINPVA 7  
DB 430 QHNPVA 436  
:|||||

Query Match 86.5%; Score 32; DB 1; Length 716;

Best Local Similarity 85.7%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

DB 430 QHNPVA 436

## RESULT 4

ID RRPO\_TNVA STANDARD; PRT; 723 AA.

AC P22958;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) [CONTAINS: 23 KDA PROTEIN].

OS Tobacco necrosis virus (strain A) (TNV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;

OC Necrovirus.

OX NCBI\_TaxID=12055;

RT [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=90320143; PubMed=2371773;

RA Meulwaeter F., Seurinck J., van Emmelo J.;

RT "Genome structure of tobacco necrosis virus strain A";

RL Virology 177:699-709(1990).

CC -I- MISCELLANEOUS: READTHROUGH OF A TERMINATOR CODON OCCURS BETWEEN

CC CODONS FOR LYS-202 AND GLY-203.

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RESULT 8
GRQ_LYMS  STANDARD; PRT; 353 AA.
AC P38411;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95324523; PubMed=7601100;
RA Klotz J.C., Ramatasingh S., van Kesteren E.R., van Minnen J.,
RA Planta R.J., van Heerikhuizen H., Vreugdenhil E.;
RT "Cloning of a molluscan G protein alpha subunit of the Gq class which
RT is expressed differentially in identified neurons."
RL Eur. J. Biochem. 230:193-199(1995).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
CC -----
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CC -----
DR EMBL; Z23106; CAA80653.1; -
DR PIR; S34347; S34347.
DR HSP; P04896; IAZT.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha.1.
DR PRINTS; PR00318; GPROTEIN.
DR PRINTS; PR00442; GPROTEINQ.
DR SMART; SM00275; G-alpha.1.
DR GRP-binding; Transducer; Multigene family; ADP-ribosylation;
KW Palmitate; Lipoprotein.
FT LIPID 3
FT LIPID 4
FT NP_BIND 40 47
FT NP_BIND 199 203
FT NP_BIND 268 271
FT NP_BIND 177 177
FT MOD_RES 177
FT ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY)
SQ SEQUENCE 353 AA: 41565 MW; 960F7604E952A3FD CRC64;

Query Match 78.4%; Score 29; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYINP 5
DB 94 QYINP 98

RESULT 9
TRPE_ARCFU  STANDARD; PRT; 411 AA.
ID TRPE_ARCFU
AC Q28669;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
DE TRPE OR AF1603.
GN

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OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Krelavage A.R., Graham D.B., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE -> ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -!- SUBUNIT: Tetramer of two components I and two components II (by
CC similarity).
CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
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CC -----
DR EMBL; AE000992; AAB89646.1; -
DR TIGR; AF1603; -
DR InterPro; IPR000350; Chorismate_bind.
DR Pfam; PF00425; chorismate_bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.
DR PRODOM; PD000779; Chorismate_bind; 1.
DR Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 411 AA: 46346 MW; 2D65F91E5BF4457A CRC64;

Query Match 78.4%; Score 29; DB 1; Length 411;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYINPV 6
DB 5 EYVNPV 10

RESULT 10
GAG2_DROME  STANDARD; PRT; 414 AA.
ID GAG2_DROME
AC P20828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE RETROVIRUS-RELATED GAG POLYPROTEIN (TRANSPON 297).
DE GAG.
GN GAG.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```

OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86108354; PubMed=2417839;  
 RA Inouye S., Yuki S., Saigo K.;  
 RT "Complete nucleotide sequence and genome organization of a *Drosophila*  
 RL transposable genetic element, 297";  
 RL Eur. J. Biochem. 154:417-425(1986).  
 CC -----  
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 CC -----  
 CC EMBL; X03431; CAA27159.1;  
 DR PIR; A24872; A24872;  
 DR FlyBase; F8gn000005; 297.  
 KW Core protein; Polyprotein; Transposable element.  
 SQ SEQUENCE 414 AA; 49250 MW; 7393C9CEE864148 CRC64;  
  
 Query Match 78.4%; Score 29; DB 1; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 73;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 QYINP 5  
 Db 274 QYINP 278  
  
 RESULT 11  
 ID YAS2\_SCHPO STANDARD; PRT; 444 AA.  
 AC Q10138;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HYPOTHETICAL 51.5 KDA PROTEIN C3H8.02 IN CHROMOSOME I.  
 GN SPAC3H8.02.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Gencies S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; Z69086; CAA93159.1;  
 DR InterPro; IPR001251; CRAL TRIO.  
 DR Pfam; PF00650; CRAL TRIO; 1.  
 DR SMART; SM00516; SEC14; 1.  
 KW Hypothetical protein.  
 FT DOMAIN 52 57 POLY-SER.  
 SQ SEQUENCE 444 AA; 51473 MW; 95C4DC7AESA2E27D CRC64;

Query Match 78.4%; Score 29; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 QYINP 5  
 Db 311 QYINP 315  
  
 RESULT 12  
 ID YBXG\_BACSU STANDARD; PRT; 462 AA.  
 AC P54425; O31438;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1).  
 GN YBXG OR YBDP.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;  
 RT "Sequence analysis of the 70kb region between 17 and 23 degree of the  
 RL Bacillus subtilis chromosome";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 339-462 FROM N.A.  
 RC STRAIN=168 / PY79;  
 RX MEDLINE=97169156; PubMed=9016963;  
 RA Sheptov M., Chyu G., Bagyan L., Cutting S.M.;  
 RT "Characterization of csGA, a new member of the forespore-expressed  
 RL sigmaag-regulon from Bacillus subtilis";  
 RL Gene 184:133-140(1997).  
 CC -!- FUNCTION: PROBABLE AMINO-ACID OR METABOLITE TRANSPORT PROTEIN.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AB005424; BAA33104.1;  
 DR EMBL; X92859; CAA63442.1;  
 DR EMBL; Z99105; CAB12000.1;  
 DR Subtilist; BG11505; ybxg.  
 DR InterPro; IPR002293; AA\_rel\_permease\_1.  
 DR InterPro; IPR002027; Amino\_acid\_permease.  
 DR Pfam; PF00324; aa\_permeases; 1.  
 DR PROSITE; PS00218; AMINO\_ACID\_PERMEASE\_1; 1.  
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;  
 Complete proteome.  
 FT TRANSMEM 17 37 POTENTIAL.  
 FT TRANSMEM 38 58 POTENTIAL.  
 FT TRANSMEM 89 109 POTENTIAL.  
 FT TRANSMEM 121 141 POTENTIAL.  
 FT TRANSMEM 154 174 POTENTIAL.  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT TRANSMEM 276 296 POTENTIAL.  
 FT TRANSMEM 331 351 POTENTIAL.  
 FT TRANSMEM 355 375 POTENTIAL.  
 FT TRANSMEM 398 418 POTENTIAL.  
 FT TRANSMEM 427 447 POTENTIAL.  
 FT TRANSMEM 439 462 POTENTIAL.  
 FT CONFLICT 339 363 IGLAVGVLYNIAPPKLFVYVYSAS -> DRFGCRRCCTELY  
 RAEDLCICLQRN (IN REF. 2).  
 SQ SEQUENCE 462 AA; 50109 MW; C4CC1787D650952C CRC64;

Query Match 78.4%; Score 29; DB 1; Length 462;  
 Best Local Similarity 71.4%; Pred. No. 81;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYINPVA 7  
 |||||:  
 Db 80 OYHPMA 86  
 |||||:  
 RESULT 13  
 YBF4\_YEAST  
 ID YBF4\_YEAST STANDARD; PRT; 525 AA.  
 AC P34219;  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 35, Last annotation update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 59.2 KDA PROTEIN IN PTC3-SAS3 INTERGENIC REGION.  
 GN YBL054H OR YBL0513 OR YBL0509.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RA MEDLINE=94205266; PubMed=8154187;  
 RX Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;  
 RT "Sequencing and functional analysis of a 32,560 bp segment on the  
 left arm of yeast chromosome II. Identification of 26 open reading  
 frames, including the KIP1 and SEC17 genes.";  
 RL Yeast 9:1355-1371(1993).  
 CC -1- SIMILARITY: STRONG, TO YEAST YER088C.  
 CC -----  
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 CC -----  
 CC EMBL: Z32261; CAA80793.1; -;  
 DR EMBL; Z35815; CAA84874.1; -;  
 DR PIR; S39834; S39834.  
 DR PIR; S37335; S37335.  
 DR HSSP; P06876; 1MBF.  
 DR SGD; S0000150; YBL054W.  
 DR InterPro: IPR001005; Myb\_DNA\_bind.  
 DR Pfam; PF00249; myb\_DNA-binding; 1.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS50090; MYB\_3; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 525 AA; 59226 MW; 8663DFE2641AA72E CRC64;

Query Match 78.4%; Score 29; DB 1; Length 525;  
 Best Local Similarity 66.7%; Pred. No. 93;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 YINPVA 7  
 |||||:  
 Db 360 YLNPIA 365  
 |||||:  
 RESULT 14  
 TEX\_BORPE  
 ID TEX\_BORPE STANDARD; PRT; 791 AA.  
 AC Q45388;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE TEX PROTEIN.

GN Bordetella pertussis.  
 OS Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;  
 OC Bordetella.  
 OX NCBI\_TaxID=520;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TOHAMA I;  
 RX MEDLINE=96345608; PubMed=8755871;  
 RA Fuchs T.M., Depisch H., Scarlato V., Gross R.;  
 RT "A new gene locus of Bordetella pertussis defines a novel family of  
 prokaryotic transcriptional accessory proteins.";  
 RL J. Bacteriol. 178:4445-4452(1996).  
 CC -1- FUNCTION: TRANSCRIPTION ACCESSORY PROTEIN. EXACT FUNCTION NOT  
 CC KNOWN.  
 CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: X95386; CAA64672.1; -;  
 DR HSSP; P05055; 1SRQ.  
 DR InterPro: IPR003029; S1.  
 DR Pfam; PF00575; S1; 1.  
 DR SMART; SM00316; S1; 1.  
 DR RNA-binding.  
 KW DOMAIN 570 739 S1 MOTIF.  
 FT SEQUENCE 791 AA; 85727 MW; F5185AB010294FFD CRC64;  
 SQ  
 Query Match 78.4%; Score 29; DB 1; Length 791;  
 Best Local Similarity 71.4%; Pred. No. 14c+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 OYINPVA 7  
 |||||:  
 Db 157 OYLNPEA 163  
 |||||:  
 RESULT 15  
 T2D2\_YEAST  
 ID T2D2\_YEAST STANDARD; PRT; 1407 AA.  
 AC P23255;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE TRANSCRIPTION INITIATION FACTOR TFIID 150 KDA SUBUNIT (TAFII-150)  
 DE (TSMI PROTEIN) (TSM-1).  
 GN TSMI OR TAF150 OR YCR042C OR YCR42C OR YCR724.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=92160397; PubMed=1789011;  
 RA Jaquet M., Buhler J.-M., Iborra F., Francinques-Gaillard M.-C.,  
 RA Soustelle C.;  
 RT "The MAT locus revisited within a 9.8 kb fragment of chromosome III  
 containing BUD5 and two new open reading frames.";  
 RL Yeast 7:881-888(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RY570;  
 RX MEDLINE=92035068; PubMed=1840512;  
 RA Ray B.L., White C.I., Haber J.E.;  
 RT "The TSMI gene of Saccharomyces cerevisiae overlaps the MAT locus.";  
 RL Curr. Genet. 20:25-31(1991).

```

Query Match      70.4%; Score 29; DB 1; Length 1407;
Best Local Similarity 85.7%; Pred. NO. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QYINEVA 7
DB 370 QIINEVA 376

```

Search completed: March 9, 2002, 00:47:38  
Job time: 799 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:53 ; Search time 94.88 seconds  
(without alignments)  
10.792 Million cell updates/sec

Title: US-09-922-067-10  
Perfect score: 37  
Sequence: 1 QVINPVA 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.17:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	86.5	341	10 Q9XGV4	Q9xgv4 brassica na
2	32	86.5	441	10 Q9SLD2	Q9sls2 arabidopsis
3	32	86.5	501	10 Q9M4V2	Q9m4v2 brassica na
4	32	86.5	503	10 Q9XGR5	Q9xgr5 brassica na
5	32	86.5	520	10 Q9S7F2	Q9s7f2 arabidopsis
6	32	86.5	532	10 Q9SEG9	Q9seg9 nicotiana t
7	32	86.5	534	10 Q9FUL6	Q9ful6 perilla fru
8	31	83.8	349	5 Q9GRX6	Q9grx8 chironomus
9	31	83.8	513	3 Q9P8X7	Q9p8x7 aspergillus
10	31	83.8	519	5 Q9W131	Q9w131 drosophila
11	31	83.8	747	5 Q24746	Q24746 drosophila
12	31	83.8	764	3 Q42976	Q42976 schizosacch
13	31	83.8	771	2 P71602	P71602 mycobacteri
14	31	83.8	884	4 Q9UPX6	Q9upx6 homo sapien
15	31	83.8	1417	2 Q9HWR8	Q9hwr8 pseudomonas
16	31	83.8	1498	3 Q9P884	Q9p884 emerlicella
17	30	81.1	149	2 P73048	P73048 synethocyst
18	30	81.1	178	13 Q93594	Q93594 dicentrarch
19	30	81.1	219	13 Q91036	Q91036 gadus morhu

20	30	81.1	237	13 Q91515	Q91515 fugu rubrip
21	30	81.1	238	13 Q9W706	Q9w7q6 paralichthy
22	30	81.1	240	13 Q98TH0	Q98th0 engraulis f
23	30	81.1	242	13 Q9W7Q7	Q9w7q7 paralichthy
24	30	81.1	248	2 Q45033	Q45033 borrelia bu
25	30	81.1	347	2 Q9S306	Q9s306 pseudomonas
26	30	81.1	420	5 Q17324	Q17324 caenorhabdi
27	30	81.1	698	2 Q9KUZ7	Q9kuz7 vibrio chol
28	30	81.1	753	5 Q26306	Q26306 drosophila
29	30	81.1	1547	3 Q9C1A0	Q9c1a0 aspergillus
30	29	78.4	76	5 Q24505	Q24505 drosophila
31	29	78.4	154	10 Q41287	Q41287 sorghum bic
32	29	78.4	173	2 Q9F3U2	Q9f3u2 pseudomonas
33	29	78.4	180	12 Q9J5H3	Q9j5h3 fowlpox vir
34	29	78.4	189	2 Q99T66	Q99t66 staphylococ
35	29	78.4	235	5 Q17378	Q17378 caenorhabdi
36	29	78.4	243	12 Q9E045	Q9e046 human immun
37	29	78.4	243	12 Q9E045	Q9e045 human immun
38	29	78.4	243	12 Q9E044	Q9e044 human immun
39	29	78.4	243	12 Q9E043	Q9e043 human immun
40	29	78.4	243	12 Q9E042	Q9e042 human immun
41	29	78.4	295	10 Q82796	Q82796 arabidopsis
42	29	78.4	364	5 Q9VXJ5	Q9v285 arabidopsis
43	29	78.4	411	10 Q46322	Q46322 drosophila
44	29	78.4	421	2 Q9KTA2	Q9kta2 graciaria
45	29	78.4	421	2 Q9KTA2	Q9kta2 vibrio chol

ALIGNMENTS

RESULT 1  
Q9XGV4 ID Q9XGV4 PRELIMINARY; PRT; 341 AA.  
AC Q9XGV4;  
DT 01-NOV-1999 (TREMREL. 12, Created)  
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)  
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).  
GN DGAT2.  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. JET NEUF;  
RA Nykiforuk C.L., Laroche A., Weselake R.J.;  
RT "A novel full length cDNA exhibiting high homology to diacylglycerol  
acyltransferase (DGAT) in a microspore-derived cell suspension culture  
from Brassica napus cv. Jet Neuf."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF15224; AA040881.1;  
DR InterPro; IPR003688; ACAT.  
DR Pfam; PF01800; ACAT; 1.  
KW Transferase; Acyltransferase.  
SQ SEQUENCE 341 AA; 39532 MW; 1A46340C49F16332 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 341;  
Best Local Similarity 83.3%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVINPV 6  
| | | | |  
DB 152 QVINPI 157

RESULT 2  
Q9SLD2 ID Q9SLD2 PRELIMINARY; PRT; 441 AA.  
AC Q9SLD2;

DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE DIACYLGLYCEROL O-ACYLTRANSFERASE.  
 GN AT2G19450.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLOMBIA; PubMed=10617197;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";  
 RL Nature 402:761-768(1999).  
 DR EMBL; AC005917; AAD10144.1; -;  
 DR InterPro; IPR002688; ACAT.  
 DR Pfam; PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 441 AA; 49614 MW; 9E13D1C70539182F CRC64;

Query Match 86.5%; Score 32; DB 10; Length 441;  
 Best Local Similarity 83.3%; Pred. No. 79;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 269 QYINPI 274

RESULT 3  
 Q9M4V2 PRELIMINARY; PRT; 501 AA.  
 ID Q9M4V2  
 AC Q9M4V2  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COMMANCHE;  
 RA Brown A.P., Schierer T.P., Slabas A.R.;  
 RT "Characterization of a putative diacylglycerol acyltransferase cDNA  
 RT from Brassica napus embryo.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF251794; AAF64065.1; -;  
 DR InterPro; IPR002688; ACAT.  
 DR Pfam; PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 501 AA; 57538 MW; 29E022B278D50822 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 501;  
 Best Local Similarity 83.3%; Pred. No. 92;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 312 QYINPI 317

RESULT 4  
 Q9XGR5 PRELIMINARY; PRT; 503 AA.  
 ID Q9XGR5  
 AC Q9XGR5  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).  
 GN DGAT1.  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CULTIVAR JET NEUF;  
 RA Nykiforuk C.L., Laroche A., Weselake R.J.;  
 RT "A cDNA exhibiting high homology to diacylglycerol acyltransferase  
 RT (DGAT) in a microspore-derived cell suspension culture from Brassica  
 RL napus cv. Jet Neuf";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF164434; AAD45536.1; -;  
 DR InterPro; IPR002688; ACAT.  
 DR Pfam; PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 503 AA; 56931 MW; 2B578A16FE0AD758 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 503;  
 Best Local Similarity 83.3%; Pred. No. 92;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 314 QYINPI 319

RESULT 5  
 Q9S7F2 PRELIMINARY; PRT; 520 AA.  
 ID Q9S7F2  
 AC Q9S7F2  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE DIACYLGLYCEROL ACYLTRANSFERASE.  
 GN DGAT OR DAGAT.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zou J., Wei Y., Jiao C., Selvaraj G., Taylor D.C.;  
 RT "The Arabidopsis thaliana TAG1 gene encodes for a diacylglycerol  
 RT acyltransferase.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLOMBIA; TISSUE=HYPOCOTYL;  
 RX MEDLINE=20069349; PubMed=10601854;  
 RA Bouvier-Nave P., Benveniste P., Oelkers P., Sturley S.L., Schaller H.;  
 RT "Expression in yeast and tobacco of plant cDNAs encoding acyl  
 RT CoA:diacylglycerol acyltransferase.";  
 RL Eur. J. Biochem. 267:85-96(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99313150; PubMed=10386579;  
 RT Hills M.J., Lu C., Hobbs D.H.;  
 RT "Cloning of a cDNA encoding diacylglycerol acyltransferase from

RT Arabidopsis thaliana and its functional expression.\*;  
 RL FEBS Lett. 452:145-149(1999).  
 DR EMBL; AJ238008; CAB45373.1; -.  
 DR EMBL; AF051849; AAF19262.1; -.  
 DR EMBL; AJ131831; CAB44774.1; -.  
 DR InterPro: IPR002688; ACAT.  
 DR Pfam: PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 520 AA; 58985 MW; 9CD0E3E8956CEFF4 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 520;  
 Best Local Similarity 83.3%; Pred. No. 96;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 331 QYINPI 336

RESULT 6  
 Q9SEG9 PRELIMINARY; PRT; 532 AA.  
 ID Q9SEG9  
 AC Q9SEG9  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE DIACYLGLYCEROL ACYLCOA ACYLTRANSFERASE.  
 GN DAGAT.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-CV. XANTHI SH6; TISSUE-CALLI DERIVED FROM LEAF PROTOPLASTS;  
 RX MEDLINE=20069349; PubMed=10601854;  
 RA Bouvier-Nave P., Benveniste P., Oelkers P., Sturley S.L., Schaller H.;  
 RT "Expression in yeast and tobacco of plant cDNAs encoding acyl  
 CoA:diacylglycerol acyltransferase.\*;  
 RL Eur. J. Biochem. 267:85-96(2000).  
 DR EMBL; AF129003; AAF19345.1; -.  
 DR InterPro: IPR002688; ACAT.  
 DR Pfam: PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 532 AA; 60867 MW; C9D316E7A8799310 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 532;  
 Best Local Similarity 83.3%; Pred. No. 98;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 342 QYINPI 347

RESULT 7  
 Q9FUL6 PRELIMINARY; PRT; 534 AA.  
 ID Q9FUL6  
 AC Q9FUL6  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE DIACYLGLYCEROL ACYLTRANSFERASE.  
 GN DGAT1.  
 OS Perilla frutescens.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.  
 OX NCBI\_TaxID=48386;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. OKDONG;  
 RA Hwang S., Hwang Y.;  
 RT "Isolation of Perilla frutescens diacylglycerol acyltransferase  
 cDNA.\*;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF298815; AAG33696.1; -.  
 DR InterPro: IPR002688; ACAT.  
 DR Pfam: PF01800; ACAT; 1.  
 KW Transferase; Acyltransferase.  
 SQ SEQUENCE 534 AA; 61205 MW; 8PFC173E06E5BB70 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 534;  
 Best Local Similarity 83.3%; Pred. No. 99;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 344 QYINPI 349

RESULT 8  
 Q9GRX8 PRELIMINARY; PRT; 349 AA.  
 ID Q9GRX8  
 AC Q9GRX8  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE RAE1.  
 OS Chironomus tentans (Midge).  
 GN Chironomus tentans (Midge).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;  
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.  
 OX NCBI\_TaxID=7153;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Sabri N., Visa N.;  
 RT "Interaction of Ct-RAE1 with Balbiani ring RNP particles during  
 nuclear export occurs at the nuclear pore.\*;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ277787; CAC14665.1; -.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 4.  
 DR PRINTS; PR00320; GPROTEINRPT.  
 DR SMART; SM00320; WD40; 4.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 DR PROSITE; PS0082; WD\_REPEATS\_2; 3.  
 DR PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat.  
 SQ SEQUENCE 349 AA; 39322 MW; EF475B9EEDC19411 CRC64;

Query Match 83.8%; Score 31; DB 5; Length 349;  
 Best Local Similarity 83.3%; Pred. No. 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6  
 |||||  
 Db 227 QYINPV 232

RESULT 9  
 Q9P8X7 PRELIMINARY; PRT; 513 AA.  
 ID Q9P8X7  
 AC Q9P8X7  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEXOSE TRANSPORTER PROTEIN.  
 GN HXTA.  
 OS Aspergillus parasiticus.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eutriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 RN NCBI\_TaxID=5067;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SU-1;  
 RA Yu J.;  
 RT "Cloning of sugar utilization pathway gene cluster in Aspergillus  
 parasiticus";  
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.  
 DR EMBL: AF168613; AAF26273.1; -.  
 DR InterPro: IPR003662; sub.transporter.  
 DR Pfam: PF00083; sugar\_tr; 1.  
 DR PROSITE: PS00216; SUGAR\_TRANSPORT\_1; UNKNOWN\_2.  
 KW Transmembrane.  
 SQ SEQUENCE 513 AA; 55986 MW; 0C7EDF709AD7DAA5 CRC64;

Query Match 83.8%; Score 31; DB 3; Length 513;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 I::I::I  
 Db 430 QFVNPIA 436

RESULT 10  
 Q9W131 PRELIMINARY; PRT; 519 AA.  
 AC Q9W131;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CG13594 PROTEIN (FRAGMENT).  
 GN CG13594.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Boldtaker P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003464; AAF47246.1; -.  
 DR FlyBase: FBgn0035041; CG13594.  
 DR NON TPR 519  
 FT SEQUENCE 519 AA; 53915 MW; F9B3C22A61245D3B CRC64;

Query Match 83.8%; Score 31; DB 5; Length 519;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7  
 I::I::I  
 Db 219 YVNPVA 224

RESULT 11  
 Q24746 PRELIMINARY; PRT; 747 AA.  
 ID Q24746;  
 AC Q24746;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE NEURALIZED PROTEIN.  
 GN NEUR OR NEU.  
 OS Drosophila virilis (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7244;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95095077; PubMed=6001814;  
 RA Zhou L., Boulianne G.L.;  
 RT "Comparison of the neuralized genes of Drosophila virilis and D.  
 melanogaster";  
 RL Genome 37:840-847(1994).  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL: U12593; AAB60619.1; -.  
 DR EMBL: U12591; AAB60619.1; JOINED.  
 DR EMBL: U12592; AAB60619.1; JOINED.  
 DR FlyBase: FBgn0013132; Dvir\neur.  
 DR InterPro: IPR001841; znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 747 AA; 81982 MW; C8E72569D6FDCAll CRC64;

Query Match 83.8%; Score 31; DB 5; Length 747;  
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
 I::I::I  
 Db 661 QYIEPVA 667

RESULT 12  
 O42976 PRELIMINARY; PRT; 764 AA.  
 ID O42976  
 AC O42976;



01-JAN-1999 (TRENBLREL. 09, Created)  
01-JAN-1999 (TRENBLREL. 09, Last sequence update)  
01-MAR-2001 (TRENBLREL. 16, Last annotation update)  
HYPOTHETICAL 85.4 KDA PROTEIN C20F10.07 IN CHROMOSOME II.  
SPC20F10.07.  
Schizosaccharomyces pombe (Fission yeast).  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.  
NCBI\_TaxID=4896;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=972;  
Lyne M., McDougall R., Rajandream M.A., Barrell B.G., Beck A.,  
Reinhardt R.,  
Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
-!- SIMILARITY: SOME, TO YEAST YHR080C.  
EMBL; AL021747; CAA16847.1; -.  
Hypothetical protein.  
KW  
SEQUENCE 764 AA; 85354 MW; 080990E5C7FA47B2 CRC64; 5

Query Match 83.8%; Score 31; DB 3; Length 764;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7  
||| |||  
Db 489 QYIKPVA 495

RESULT 13  
ID P71602 PRELIMINARY; PRT; 771 AA.  
AC P71602;  
DT 01-JAN-1998 (TRENBLREL. 05, Created)  
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE HYPOTHETICAL 86.2 KDA PROTEIN CY10H4.32.  
GN RV0032 OR MTCV10H4.32.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=H37RV;  
Murphy L., Harris D., Barrell B.G., Rajandream M.A.;  
Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
-!- SIMILARITY: TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES,  
DR HSP; P12998; 1BS0.  
DR Tuberculin; RV0032; -.  
DR InterPro; IPR001917; AminoTransf\_2.  
DR Pfam; PF00222; aminotran\_2; 1.  
DR PROSITE; PS00599; AA\_TRANSF\_2; UNKNOWN\_1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 771 AA; 86242 MW; 8FCID0FED27E43C6 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 771;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7  
||| |||  
Db 721 YINPVA 726

RESULT 14  
ID Q9UPX6 PRELIMINARY; PRT; 884 AA.

01-MAY-2000 (TRENBLREL. 13, Created)  
01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE KIAA1024 PROTEIN (FRAGMENT).  
GN KIAA1024.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=BRAIN;  
MEDLINE=99397452; PubMed=10470851;  
Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,  
Tanaka A., Kohani H., Nomura N., Ohara O.;  
"Prediction of the coding sequences of unidentified human genes. XIV.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro.";  
DNA Res. 6:197-205(1999).  
EMBL; AB028947; BAA82976.1; -.  
InterPro; IPR002106; AA\_TRNA\_ligase\_II.  
DR PROSITE; PS00339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 884 AA; 99289 MW; 4594A37B0CF3C7B4 CRC64;

Query Match 83.8%; Score 31; DB 4; Length 884;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6  
||| |||  
Db 279 QYINPV 284

RESULT 15  
ID Q9HWR8 PRELIMINARY; PRT; 1417 AA.  
AC Q9HWR8; (TRENBLREL. 16, Created)  
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE PROBABLE SENSOR/RESPONSE REGULATOR HYBRID.  
GN PA4112.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=PA01;  
MEDLINE=20437337; PubMed=10984043;  
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
Brody L.L., Coulter S.N., Folger K.B., Kas A., Larbig K., Lim R.M.,  
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
"Complete genome sequence of Pseudomonas aeruginosa PA01, an  
opportunistic pathogen.";  
Nature 406:959-964(2000).  
RL Nature 406:959-964(2000).  
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER  
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.  
CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE  
CC KINASES.  
EMBL; AE004827; AAG07499.1; -.  
DR InterPro; IPR000410; Bctrl\_sens.  
DR InterPro; IPR003594; HATPase\_C.  
DR InterPro; IPR003661; His\_kinA.  
DR InterPro; IPR002570; Hpt.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000014; PAS.

DR InterPro: IPR000700; PAS-assoc\_C.  
 DR InterPro: IPR001789; Response\_reg.  
 DR Pfam: PF02518; HATPase\_C; 1.  
 DR Pfam: PF00785; PAC; 3.  
 DR Pfam: PF00989; PAS; 2.  
 DR Pfam: PF00072; response\_reg; 2.  
 DR Pfam: PF00512; signal; 1.  
 DR PRINTS: PR00344; BCTRLSENSOR.  
 DR SMART: SM00387; HATPase\_C; 1.  
 DR SMART: SM00388; HSKA; 1.  
 DR SMART: SM00073; HPT; 1.  
 DR SMART: SM00086; PAC; 3.  
 DR SMART: SM00091; PAS; 3.  
 DR SMART: SM00448; REC; 2.  
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;  
 KW Transference.  
 SQ SEQUENCE 1417 AA; 153893 MW; 224E2EC9B45EAF2B CRC64;

Query Match 83.8%; Score 31; DB 2; Length 1417;  
 Best Local Similarity 85.7%; Pred. No. 5c+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QYINPVA 7  
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 DB 147 QYIEPVA 153

Search completed: March 9, 2002, 00:46:55  
 Job time: 831 sec

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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 Seconds  
(without alignments)  
12.939 Million cell updates/sec

Title: US-09-922-067-11  
Perfect score: 104  
Sequence: 1 MITIRKSHQNPADTFATG 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	20	16 AAR64930	Human lipoprotein-
2	104	100.0	27	16 AAR64929	Human lipoprotein-
3	104	100.0	440	22 AAE00782	Mouse-human plasma
4	104	100.0	440	22 AAE00783	Mouse-human plasma
5	104	100.0	441	16 AAR73048	Human acetyl hydro
6	104	100.0	441	16 AAR73049	Human acetyl hydro
7	104	100.0	441	16 AAR73050	Human acetyl hydro
8	104	100.0	441	16 AAR71920	Human acetyl hydro
9	104	100.0	441	16 AAR71921	Human acetyl hydro
10	104	100.0	441	16 AAR71922	Human acetyl hydro
11	104	100.0	441	16 AAR71923	Human acetyl hydro

12	104	100.0	441	16 AAR71925	Human acetyl hydro
13	104	100.0	441	16 AAR73046	Human acetyl hydro
14	104	100.0	441	16 AAR73047	Human plasma plate
15	104	100.0	441	16 AAR71913	Human platelet-act
16	104	100.0	441	18 AAW26498	Human plasma plate
17	104	100.0	441	18 AAW23796	Platelet-activatin
18	104	100.0	441	18 AAW09808	Human plasma plate
19	104	100.0	441	19 AAW38361	Human plasma plate
20	104	100.0	441	20 AAW66334	Human PAF-AH prote
21	104	100.0	441	20 AAW73359	Plasma platelet-ac
22	104	100.0	441	21 AAB07774	Human low density
23	104	100.0	441	21 AAB01942	Human platelet-act
24	104	100.0	441	21 AAY88301	Human PAF-AH prote
25	104	100.0	441	21 AAY50735	Human plasma plate
26	104	100.0	441	22 AAE00761	Human plasma plate
27	104	100.0	441	22 AAE00768	Human plasma plate
28	104	100.0	441	22 AAE00769	Human plasma plate
29	104	100.0	441	22 AAE00770	Human plasma plate
30	104	100.0	441	22 AAE00771	Human plasma plate
31	104	100.0	441	22 AAE00772	Human plasma plate
32	104	100.0	441	22 AAE00773	Human plasma plate
33	104	100.0	441	22 AAE00774	Human platelet-act
34	104	100.0	441	22 AAE00776	Human plasma plate
35	104	100.0	441	22 AAE00777	Human plasma plate
36	104	100.0	441	22 AAE00778	Human plasma plate
37	104	100.0	441	22 AAE00779	Human plasma plate
38	104	100.0	441	22 AAE00780	Human plasma plate
39	104	100.0	441	22 AAE00781	Human plasma plate
40	104	100.0	441	22 AAB49451	Platelet-activatin
41	104	100.0	442	16 AAR64928	Human T-cell lymph
42	100	96.2	444	16 AAR71915	Canine platelet ac
43	100	96.2	444	18 AAW26501	Canine platelet-ac
44	100	96.2	444	18 AAW23798	Canine plasma plat
45	100	96.2	444	18 AAW09810	Canine platelet-ac

ALIGNMENTS

RESULT 1  
AAR64930  
ID AAR64930 standard; Peptide; 20 AA.  
AC AAR64930;  
XX 18-AUG-1995 (first entry)  
XX Human lipoprotein-associated phospholipase-A2 peptide-6.  
XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;  
XX enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.  
XX Homo sapiens.  
OS WO9500649-A.  
PN 05-JAN-1995.  
PD 24-JUN-1994; 94WO-GB01374.  
PF 25-JUN-1993; 93GB-0013144.  
PR 11-JAN-1994; 94GB-0000413.  
XX (SMK ) SMITHKLINE BEECHAM PLC.  
XX Gloger IS, Hickey DMB, Lawrence GMP, Macphee CH;  
XX Rice SQJ, Southan CD, Tew DG;  
XX WPI: 1995-052086/07.  
XX Purified lipoprotein associated phospholipase A2 - used to develop prods. for diagnosis and therapy, partic. inhibitors for treatment of atherosclerosis

XX Claim 9; Page 21; 29pp; English.  
 XX  
 CC This sequence encodes a peptide fragment of an enzyme which may be  
 CC used in a method of screening compounds to identify those compounds  
 CC which inhibit Lp-PLA2 which involves contacting isolated Lp-PLA2  
 CC with a test compound and measuring the rate of turnover of an  
 CC enzyme substrate as compared with the rate of turnover of an  
 CC absence of the test compound.  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 104; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-12;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSHVHQNFADEFTATG 20  
 Db 1 mitirgshvhnqnfadftatg 20

RESULT 2  
 AAR64929  
 ID AAR64929 standard; Peptide; 27 AA.  
 AC AAR64929;

DT 18-AUG-1995 (first entry)

DE Human lipoprotein-associated phospholipase-A2 peptide-3.

XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;  
 KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.  
 XX  
 OS Homo sapiens.

XX WO9500649-A.

PN 05-JAN-1995.

PD 24-JUN-1994; 94WO-GB01374.

PR 25-JUN-1993; 93GB-0013144.

XX 11-JAN-1994; 94GB-0000413.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gloger IS, Hickey DMB, Lawrence GMP, Macphee CH;

PI Rice SQJ, Southan CD, Tew DG;

XX WPI; 1995-052086/07.

XX Purified lipoprotein-associated phospholipase A2 - used to  
 PT develop prods. for diagnosis and therapy, partic. inhibitors for  
 PT treatment of atherosclerosis

XX Claim 9; Page 17; 29pp; English.

XX This sequence encodes a peptide fragment of an enzyme which may be  
 CC used in a method of screening compounds to identify those compounds  
 CC which inhibit Lp-PLA2 which involves contacting isolated Lp-PLA2  
 CC with a test compound and measuring the rate of turnover of an  
 CC enzyme substrate as compared with the rate of turnover of an  
 CC absence of the test compound.

XX Sequence 27 AA;

Query Match 100.0%; Score 104; DB 16; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSHVHQNFADEFTATG 20  
 Db 8 mitirgshvhnqnfadftatg 27

RESULT 3

AE00782  
 ID AAE00782 standard; Protein; 440 AA.

XX AAE00782;

XX 02-JUL-2001 (first entry)

XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHCl.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
 KW antiinflammatory; septicaemia; inflammation; haemostasis; purpuration;  
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

OS Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Region

FT 1..97 /note= "Corresponds to N-terminal 97 amino acids of mouse  
 plasma platelet-activating factor acetylhydrolase  
 (PAF-AH)"

FT 98..440

FT Region

FT /note= "Corresponds to C-terminal 343 amino acids of  
 human plasma platelet-activating factor acetylhydrolase  
 (PAF-AH)"

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

XX 22-JAN-1998; 98US-0010715.

XX 06-OCT-1993; 93US-0133603.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

XX Wilder CL;

XX WPI; 2001-280610/29.

XX N-PSDB; AAD04168.

XX Treating a mammal susceptible to or suffering from septicemia comprises  
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to  
 PT supplement endogenous PAF-AH activity and to inactivate pathological  
 PT amounts of PAF

XX Example 8; Column -; 54pp; English.

XX The present sequence is mouse-human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid  
 CC pRC/PH.MHCl.

XX The invention relates to human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The  
 CC invention also relates to method of treating a mammal susceptible to  
 CC or suffering from septicemia. PAF functions in normal physiological  
 CC processes such as inflammation, haemostasis and purpuration. PAF-AH  
 CC specific antibodies are used in the diagnostic methods to detect abnormal  
 CC levels of PAF-AH in serum and also for treating the pathological  
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic  
 CC shock and arthritis. PAF-AH antibody is also useful for screening a  
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the  
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting  
 CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human  
 CC plasma PAF-AH gene.  
 XX  
 SQ sequence 440 AA;

Query Match 100.0%; Score 104; DB 22; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MITIRGSVHQNFAADFTFATG 20  
 |||||  
 Db 342 mitirgsvhqnfnadftfatg 361

RESULT 4  
 AA000783  
 ID AA000783 standard; Protein: 440 AA.  
 XX  
 AC AA000783;  
 XX  
 DT 02-JUL-2001 (first entry)  
 XX  
 DE Mouse-human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.  
 KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;  
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;  
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 XX

Key Location/Qualifiers  
 Region 1..40  
 /note= "corresponds to N-terminal 40 amino acids of mouse plasma platelet-activating factor acetylhydrolase (PAF-AH)"  
 Region 41..440  
 /note= "Corresponds to C-terminal 400 amino acids of human plasma platelet-activating factor acetylhydrolase (PAF-AH)"

US6203790-B1.  
 20-MAR-2001.  
 23-MAY-2000; 2000US-0577758.  
 07-JUN-1995; 95US-0480658.  
 22-JAN-1998; 98US-0010715.  
 06-OCT-1993; 93US-0133803.  
 06-OCT-1994; 94US-0318905.  
 (ICOS-) ICOS CORP.  
 Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;  
 Wilder CL;  
 WPI; 2001-280610/29.  
 N-PSDB: AAD04169.

Treating a mammal susceptible to or suffering from septicemia comprises administering a platelet-activating factor acetyl hydrolase (PAF-AH) to supplement endogenous PAF-AH activity and to inactivate pathological amounts of PAF.

Example 8; Column 7; 54pp; English.  
 The present sequence is mouse-human plasma platelet-activating factor acetylhydrolase (PAF-AH) fusion protein construct from plasmid pRC/PH.MHC2.  
 The invention relates to human plasma platelet-activating factor acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to or suffering from septicemia. PAF functions in normal physiological processes such as inflammation, haemostasis and parturition. PAF-AH specific antibodies are used in the diagnostic methods to detect abnormal levels of PAF-AH in serum and also for treating the pathological inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic shock and arthritis. PAF-AH antibody is also useful for screening a genetic lesion in the human plasma PAF-AH gene, which occurs due to the replacement of nucleotide G to T at position 996 within exon 9 resulting in replacement of amino acid Val to Phe at position 279. Thus the deficiency of PAF-AH activity is due to the genetic lesion in human plasma PAF-AH gene.  
 XX  
 SQ Sequence 440 AA;

Query Match 100.0%; Score 104; DB 22; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MITIRGSVHQNFAADFTFATG 20  
 |||||  
 Db 342 mitirgsvhqnfnadftfatg 361

RESULT 5  
 AAR73048  
 ID AAR73048 standard; Protein: 441 AA.  
 XX  
 AC AAR73048;  
 XX  
 DT 06-DEC-1995 (first entry)  
 XX  
 DE Human acetyl hydrolase (AH) mutant C291S.  
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Misc-difference 291  
 FT /note= "Wild-type Cys is substd. by Ser."

W09509921-A.  
 13-APR-1995.  
 06-OCT-1994; 94WO-US11340.  
 06-OCT-1993; 93US-0133803.  
 (ICOS-) ICOS CORP.  
 Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 Wilder CL;  
 WPI; 1995-155262/20.  
 New nucleic acid encoding platelet activating factor,  
 acetylhydrolase - useful in diagnosis and for treating  
 inflammatory diseases, e.g. pleurisy  
 Example 10; 88pp; English.

The human acetyl hydrolase (AH) gene (AA087947) has been isolated and purified. Several mutant clones of AH (AAR71920-23 and AAR73046-49) were made with single amino acid changes for the purposes of identifying the active site of AH. The sequences of these mutants are not given in the patent specification; they have been derived from the original wild-type protein (AAR71913).  
 The AH gene and its product are useful in the treatment of inflammatory diseases, in particular pleurisy, asthma, rhinitis and eczema. The

CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.  
 XX  
 SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSHQNFADFTFATG 20  
 |||||  
 DB 343 mitirgshqnfadftfatg 362

## RESULT 6

ID AAR73049 standard; Protein; 441 AA.  
 XX  
 AC AAR73049;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C334S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.

PH Key Location/Qualifiers  
 FT Misc-difference 334 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSHQNFADFTFATG 20  
 |||||  
 DB 343 mitirgshqnfadftfatg 362

## RESULT 7

ID AAR73050 standard; Protein; 441 AA.  
 XX  
 AC AAR73050;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C407S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
 KW disease; pleurisy; diagnosis.  
 XX  
 OS Homo sapiens.

PH Key Location/Qualifiers  
 FT Misc-difference 407 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
 PT acetyl:hydrolase - useful in diagnosis and for treating  
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and  
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
 CC made with single amino acid changes for the purposes of identifying  
 CC the active site of AH. The sequences of these mutants are not given  
 CC in the patent specification; they have been derived from the original  
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
 CC gene may also be used in raising monoclonal antibodies specific for AH  
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSHQNFADFTFATG 20  
 |||||  
 DB 343 mitirgshqnfadftfatg 362

## RESULT 8

ID AAR71920 standard; Protein; 441 AA.  
 XX  
 AC AAR71920;

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XX 06-DEC-1995 (first entry)
XX Human acetyl hydrolase (AH) mutant S108A.
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 108
XX /note= "Wild-type Ser is substd. by Ala."
XX WO9509921-A.
XX 13-APR-1995.
XX 06-OCT-1994; 94WO-US11340.
XX 06-OCT-1993; 93US-0133803.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX WPI: 1995-155262/20.
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX Example 10; ; 88pp; English.
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
XX in the patent specification; they have been derived from the original
XX wild-type protein (AAR71913).
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX Sequence 441 AA;
XX
XX Query Match 100.0%; Score 104; DB 16; Length 441;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MITIRGSVHQNFADFTFATG 20
XX |||||
XX Db 343 mitirgsvhqnfadftfatg 362
XX
XX RESULT 9
XX AAR71921
XX ID AAR71921 standard; Protein; 441 AA.
XX AC AAR71921;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE Human acetyl hydrolase (AH) mutant S273A.
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX Homo sapiens.

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FH Key Location/Qualifiers
FT Misc-difference 273
FT /note= "Wild-type Ser is substd. by Ala."
XX WO9509921-A.
XX 13-APR-1995.
XX 06-OCT-1994; 94WO-US11340.
XX 06-OCT-1993; 93US-0133803.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX WPI: 1995-155262/20.
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX Example 10; ; 88pp; English.
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
XX in the patent specification; they have been derived from the original
XX wild-type protein (AAR71913).
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX Sequence 441 AA;
XX
XX Query Match 100.0%; Score 104; DB 16; Length 441;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MITIRGSVHQNFADFTFATG 20
XX |||||
XX Db 343 mitirgsvhqnfadftfatg 362
XX
XX RESULT 10
XX AAR71922
XX ID AAR71922 standard; Protein; 441 AA.
XX AC AAR71922;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE Human acetyl hydrolase (AH) mutant D296A.
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 296
XX /note= "Wild-type Asp is substd. by Ala."
XX WO9509921-A.
XX 13-APR-1995.
XX 06-OCT-1994; 94WO-US11340.
XX

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PR 06-OCT-1993; 93US-0133803.  
XX (ICOS-) ICOS CORP.  
XX

PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;  
XX

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy  
XX

PS Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADTFATG 20  
Db ||||||||||||||||  
343 mitirgsvhqnfadtfatg 362

RESULT 11

AAR71923  
ID AAR71923 standard; Protein; 441 AA.

AC AAR71923;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant D338A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 338

FT /note= "Wild-type Asp is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;  
XX

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy  
XX

PS Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADTFATG 20  
Db ||||||||||||||||  
343 mitirgsvhqnfadtfatg 362

RESULT 12

AAR71925  
ID AAR71925 standard; Protein; 441 AA.

AC AAR71925;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant H395A/H399A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
KW disease; pleurisy; diagnosis.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 395

FT /note= "Wild-type His is substd. by Ala."

FT /note= "Wild-type His is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;  
PI Wilder CL;  
XX

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy  
XX

PS Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying



CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).  
CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSVHQNFADEFTFATG 20  
|||||  
DB 343 mitirgsvhqnfdftfatg 362

RESULT 13

AAR73046  
ID AAR73046 standard; Protein; 441 AA.

XX AC AAR73046;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant C67S.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 67

FT /note= "Wild-type Cys is substd. by Ser."

XX WO9505921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX CC Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; : 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AAO87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).  
CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSVHQNFADEFTFATG 20  
|||||  
DB 343 mitirgsvhqnfdftfatg 362

RESULT 14

AAR73047  
ID AAR73047 standard; Protein; 441 AA.

XX AC AAR73047;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant C229S.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;  
XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 229

FT /note= "Wild-type Cys is substd. by Ser."

XX PN WO9505921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX CC Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,  
PT acetyl:hydrolase - useful in diagnosis and for treating  
PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; : 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AAO87947) has been isolated and  
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were  
CC made with single amino acid changes for the purposes of identifying  
CC the active site of AH. The sequences of these mutants are not given  
CC in the patent specification; they have been derived from the original  
CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory  
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The  
CC gene may also be used in raising monoclonal antibodies specific for AH  
CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITIRGSVHQNFADEFTFATG 20  
|||||  
DB 343 mitirgsvhqnfdftfatg 362

1

Search completed: March 9, 2002, 00:31:58  
Job time: 444 sec



Query Match 100.0%; Score 104; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20  
|||||  
DB 1 MITIRGSVHONFADFTFATG 20

## RESULT 2

US-08-387-858A-11  
; Sequence 11, Application US/08387858A  
; Patent No. 5981252  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,858A  
FILING DATE: 24 February 1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCY/GB94/01374  
FILING DATE: 24 June 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-387-858A-11

Query Match 100.0%; Score 104; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20  
|||||  
DB 1 MITIRGSVHONFADFTFATG 20

## RESULT 3

US-09-294-384B-11  
; Sequence 11, Application US/09294384B  
; Patent No. 6177257  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse  
; APPLICANT: Rice, Simon Quentyn John  
; TITLE OF INVENTION: Compounds  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,384B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,858  
FILING DATE: 24 February 1995  
APPLICATION NUMBER: PCY/GB94/01374  
FILING DATE: 24 June 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-09-294-384B-11

Query Match 100.0%; Score 104; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20  
|||||  
DB 1 MITIRGSVHONFADFTFATG 20

## RESULT 4

US-08-557-892-3  
; Sequence 3, Application US/08557892  
; Patent No. 5968818  
; GENERAL INFORMATION:  
; APPLICANT: MacPhee, Colin Houston  
; APPLICANT: Tew, David Graham  
; APPLICANT: Southan, Christopher Donald  
; APPLICANT: Hickey, Dierdre Mary Bernadette  
; APPLICANT: Gloger, Israel Simon  
; APPLICANT: Lawrence, Geoffrey Mark Prouse

APPLICANT: Rice, Simon Quentyn John  
TITLE OF INVENTION: Compounds  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,892  
FILING DATE: 14 No. 5968818ember 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/387,858  
FILING DATE: 14 No. 5968818ember 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693C1  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-557-892-3

Query Match 100.0%; Score 104; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.8e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFAFFTATG 20  
|||||  
Db 8 MITIRGSVHQNFAFFTATG 27

RESULT 5  
US-08-387-858A-3  
Sequence 3, Application US/08387858A  
Patent No. 5981252  
GENERAL INFORMATION:  
APPLICANT: MacPhee, Colin Houston  
APPLICANT: Tew, David Graham  
APPLICANT: Southan, Christopher Donald  
APPLICANT: Hickey, Dierdre Mary Bernadette  
APPLICANT: Gloger, Israel Simon  
APPLICANT: Lawrence, Geoffrey Mark Prouse  
APPLICANT: Rice, Simon Quentyn John  
TITLE OF INVENTION: Compounds  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,858A  
FILING DATE: 24 February 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/01374  
FILING DATE: 24 June 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-387-858A-3

Query Match 100.0%; Score 104; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.8e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFAFFTATG 20  
|||||  
Db 8 MITIRGSVHQNFAFFTATG 27

RESULT 6  
US-09-294-384B-3  
Sequence 3, Application US/09294384B  
Patent No. 6177257  
GENERAL INFORMATION:  
APPLICANT: MacPhee, Colin Houston  
APPLICANT: Tew, David Graham  
APPLICANT: Southan, Christopher Donald  
APPLICANT: Hickey, Dierdre Mary Bernadette  
APPLICANT: Gloger, Israel Simon  
APPLICANT: Lawrence, Geoffrey Mark Prouse  
APPLICANT: Rice, Simon Quentyn John  
TITLE OF INVENTION: Compounds  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,384B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,858  
FILING DATE: 24 February 1995  
APPLICATION NUMBER: PCT/GB94/01374  
FILING DATE: 24 June 1994

ATTORNEY/AGENT INFORMATION:  
NAME: Dustman, Wayne J.  
REGISTRATION NUMBER: 33,870  
REFERENCE/DOCKET NUMBER: P30693  
TELEPHONE: 610-270-5023  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-09-294-384B-3

Query Match 100.0%; Score 104; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.8e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20  
|||||

DB 8 MITIRGSVHQNFADEFTFATG 27

RESULT 7  
US-08-470-187-8  
Sequence 8, Application US/08470187  
Patent No. 5532152

GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine E.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,187  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5532152and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-470-187-8

Query Match 100.0%; Score 104; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20  
|||||

DB 343 MITIRGSVHQNFADEFTFATG 362

RESULT 8

US-08-318-905-8  
Sequence 8, Application US/08318905  
Patent No. 5641669

GENERAL INFORMATION:  
APPLICANT: Cousens, Lawrence S.  
APPLICANT: Eberhardt, Christine D.  
APPLICANT: Gray, Patrick W.  
APPLICANT: Le Trong, Hai  
APPLICANT: Tjoelker, Larry W.  
APPLICANT: Wilder, Cheryl L.  
TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
TITLE OF INVENTION: Hydrolase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,905  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,803  
FILING DATE: 6-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5641669and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-905-8

Query Match 100.0%; Score 104; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20  
|||||

DB 343 MITIRGSVHQNFADEFTFATG 362

RESULT 9

US-08-483-232-8  
: Sequence 8, Application US/08483232  
: Patent No. 5656431  
: GENERAL INFORMATION:  
: APPLICANT: Cousens, Lawrence S.  
: APPLICANT: Eberhardt, Christine D.  
: APPLICANT: Gray, Patrick W.  
: APPLICANT: Le Trong, Hai  
: APPLICANT: Tjoelker, Larry W.  
: APPLICANT: Wilder, Cheryl L.  
: TITLE OF INVENTION: Platelet-Activating Factor  
: NUMBER OF SEQUENCES: 30  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: United States of America  
: ZIP: 60606-6402  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/483,232  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/318,905  
: FILING DATE: 06-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/133,803  
: FILING DATE: 06-OCT-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: No. 5656431and, Greta E.  
: REGISTRATION NUMBER: 35,302  
: REFERENCE/DOCKET NUMBER: 27866/32689  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (312) 474-6300  
: TELEFAX: (312) 474-0448  
: TELEX: 25-3658  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 441 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-483-232-8

Query Match 100.0%; Score 104; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MITIRGSVHONFADFTTATG 20  
Db 343 MITIRGSVHONFADFTTATG 362  
  
RESULT 10  
US-08-483-140-8  
: Sequence 8, Application US/08483140  
: Patent No. 5698403  
: GENERAL INFORMATION:  
: APPLICANT: ICOS Corporation  
: TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
: NUMBER OF SEQUENCES: 30  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: STREET: 6300 Sears Tower, 233 South Wacker Drive

: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/483,140  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/318,905  
: FILING DATE: 6-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/133,803  
: FILING DATE: 6-OCT-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: No. 5698403and, Greta E.  
: REGISTRATION NUMBER: 35,302  
: REFERENCE/DOCKET NUMBER: 32781  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (312) 474-6300  
: TELEFAX: (312) 474-0448  
: TELEX: 25-3658  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 441 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-483-140-8  
  
Query Match 100.0%; Score 104; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MITIRGSVHONFADFTTATG 20  
Db 343 MITIRGSVHONFADFTTATG 362  
  
RESULT 11  
US-08-485-938A-8  
: Sequence 8, Application US/08485938A  
: Patent No. 5847088  
: GENERAL INFORMATION:  
: APPLICANT: Cousens, Lawrence S.  
: APPLICANT: Eberhardt, Christine D.  
: APPLICANT: Gray, Patrick W.  
: APPLICANT: Le Trong, Hai  
: APPLICANT: Tjoelker, Larry W.  
: APPLICANT: Wilder, Cheryl L.  
: TITLE OF INVENTION: Platelet-Activating Factor  
: NUMBER OF SEQUENCES: 36  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: STREET: 6300 Sears Tower, 233 South Wacker Drive  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: United States of America  
: ZIP: 60606-6402  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/485,938A

;< FILING DATE: 435  
;< CLASSIFICATION: 435  
;< PRIOR APPLICATION DATA: US 08/318,905  
;< FILING DATE: 06-OCT-1994  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/133,803  
;< FILING DATE: 06-OCT-1993  
;< ATTORNEY/AGENT INFORMATION:  
;< NAME: No. 5847088and, Greta E.  
;< REGISTRATION NUMBER: 35,302  
;< REFERENCE/DOCKET NUMBER: 27866/32792  
;< TELECOMMUNICATION INFORMATION:  
;< TELEPHONE: (312) 474-6300  
;< TELEFAX: (312) 474-0448  
;< TELEX: 25-3658  
;< INFORMATION FOR SEQ ID NO: 8:  
;< SEQUENCE CHARACTERISTICS:  
;< LENGTH: 441 amino acids  
;< TYPE: amino acid  
;< TOPOLOGY: linear  
;< MOLECULE TYPE: protein  
US-08-485-938A-8

Query Match 100.0%; Score 104; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADTFTATG 20  
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Db 343 MITIRGSVHQNFADTFTATG 362

RESULT 12  
US-08-910-041-8  
;< Sequence 8, Application US/08910041  
;< Patent No. 5977308  
;< GENERAL INFORMATION:  
;< APPLICANT: Cousins, Lawrence S.  
;< APPLICANT: Eberhardt, Christine D.  
;< APPLICANT: Gray, Patrick W.  
;< APPLICANT: Le Trong, Hai  
;< APPLICANT: Tjoelker, Larry W.  
;< TITLE OF INVENTION: Platelet-Activating Factor  
;< NUMBER OF SEQUENCES: 30  
;< CORRESPONDENCE ADDRESS:  
;< ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;< STREET: 6300 Sears Tower, 233 South Wacker Drive  
;< CITY: Chicago  
;< STATE: Illinois  
;< COUNTRY: United States of America  
;< ZIP: 60606-6402  
;< COMPUTER READABLE FORM:  
;< MEDIUM TYPE: Floppy disk  
;< COMPUTER: IBM PC compatible  
;< OPERATING SYSTEM: PC-DOS/MS-DOS  
;< SOFTWARE: PatentIn Release #1.0, Version #1.25  
;< CURRENT APPLICATION DATA:  
;< APPLICATION NUMBER: US/08/910,041  
;< FILING DATE:  
;< CLASSIFICATION: 424  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/483,232  
;< FILING DATE: 07-JUN-1995  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/318,905  
;< FILING DATE: 05-OCT-1994  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/133,803  
;< FILING DATE: 06-OCT-1993

;< ATTORNEY/AGENT INFORMATION:  
;< NAME: Rin-Laures, Li-Hsien  
;< REGISTRATION NUMBER: 33,547  
;< REFERENCE/DOCKET NUMBER: 27866/34026  
;< TELECOMMUNICATION INFORMATION:  
;< TELEPHONE: (312) 474-6300  
;< TELEFAX: (312) 474-0448  
;< TELEX: 25-3658  
;< INFORMATION FOR SEQ ID NO: 8:  
;< SEQUENCE CHARACTERISTICS:  
;< LENGTH: 441 amino acids  
;< TYPE: amino acid  
;< TOPOLOGY: linear  
;< MOLECULE TYPE: protein  
US-08-910-041-8

Query Match 100.0%; Score 104; DB 2; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADTFTATG 20  
|||||  
Db 343 MITIRGSVHQNFADTFTATG 362

RESULT 13  
US-09-328-474-8  
;< Sequence 8, Application US/09328474  
;< Patent No. 6045794  
;< GENERAL INFORMATION:  
;< APPLICANT: Cousins, Lawrence S.  
;< APPLICANT: Eberhardt, Christine D.  
;< APPLICANT: Gray, Patrick W.  
;< APPLICANT: Le Trong, Hai  
;< APPLICANT: Tjoelker, Larry W.  
;< TITLE OF INVENTION: Platelet-Activating Factor  
;< NUMBER OF SEQUENCES: 30  
;< CORRESPONDENCE ADDRESS:  
;< ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;< STREET: 6300 Sears Tower, 233 South Wacker Drive  
;< CITY: Chicago  
;< STATE: Illinois  
;< COUNTRY: United States of America  
;< ZIP: 60606-6402  
;< COMPUTER READABLE FORM:  
;< MEDIUM TYPE: Floppy disk  
;< COMPUTER: IBM PC compatible  
;< OPERATING SYSTEM: PC-DOS/MS-DOS  
;< SOFTWARE: PatentIn Release #1.0, Version #1.25  
;< CURRENT APPLICATION DATA:  
;< APPLICATION NUMBER: US/09/328,474  
;< FILING DATE:  
;< CLASSIFICATION:  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/483,232  
;< FILING DATE: 07-JUN-1995  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/318,905  
;< FILING DATE: 06-OCT-1994  
;< PRIOR APPLICATION DATA:  
;< APPLICATION NUMBER: US 08/133,803  
;< FILING DATE: 06-OCT-1993  
;< ATTORNEY/AGENT INFORMATION:  
;< NAME: Rin-Laures, Li-Hsien  
;< REGISTRATION NUMBER: 33,547  
;< REFERENCE/DOCKET NUMBER: 27866/34026  
;< TELECOMMUNICATION INFORMATION:  
;< TELEPHONE: (312) 474-6300  
;< TELEFAX: (312) 474-0448  
;< TELEX: 25-3658



INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-328-474-8

Query Match 100.0%; Score 104; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADTFATG 20  
|||||  
DB 343 MITIRGSVHONFADTFATG 362

RESULT 14  
US-09-100-546-8

; Sequence 8, Application US/09100546  
; Patent No. 6099836  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,546  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/010,715  
; FILING DATE:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6099836and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32793  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-100-546-8

Query Match 100.0%; Score 104; DB 3; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADTFATG 20  
|||||  
DB 343 MITIRGSVHONFADTFATG 362

RESULT 15

US-09-010-715-8  
; Sequence 8, Application US/09010715  
; Patent No. 6146625  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/010,715  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6146625and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32793  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-010-715-8

Query Match 100.0%; Score 104; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADTFATG 20  
|||||  
DB 343 MITIRGSVHONFADTFATG 362

Search completed: March 9, 2002, 00:33:01

Mon Mar 11 10:01:54 2002

us-09-922-067-11.rai

Page 8

Job time: 402 sec

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:13 ; Search time 53.53 seconds  
(without alignments)  
28.461 Million cell updates/sec

Title: US-09-922-067-11

Perfect score: 104

Sequence: 1 MITRGSVHQNFAADFTFATG 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-68:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	104	100.0	441	2	S60247
2	86	82.7	436	2	JC5021
3	58	55.8	384	2	T32756
4	54	51.9	476	2	T28936
5	52	50.0	541	2	T47290
6	52	50.0	830	2	T47377
7	43	41.3	341	2	T32949
8	42	40.4	142	2	B40535
9	42	40.4	325	2	A28029
10	42	40.4	374	2	S69699
11	42	40.4	1230	2	H84515
12	42	40.4	1239	2	G71266
13	42	39.4	142	2	T15957
14	41	39.4	249	2	H86786
15	41	39.4	318	1	E71590
16	41	39.4	367	2	S74765
17	41	39.4	458	2	S57605
18	40	38.5	297	2	JC4398
19	40	38.5	352	2	T27607
20	40	38.5	379	2	A49679
21	40	38.5	425	2	S75024
22	40	38.5	453	2	S77558
23	40	38.5	579	2	B44857
24	40	38.5	599	2	A86810
25	40	38.5	753	2	C96668
26	40	38.5	767	2	F64605
27	40	38.5	767	2	T71909
28	40	38.5	841	1	S24462
29	39.5	38.0	213	2	T35433

thiamin-phosphate  
annexin VI - rat  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable iron-chel  
intelectin - mouse  
hypothetical prote  
heme d1 biosynthes  
preprotein translo  
coproporphyrinogen  
probable amino aci  
probable WFS trans  
hypothetical prote  
glutamate decarbox  
acetolactate synth

## ALIGNMENTS

### RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; MID:g780132; PIDN:AA50126.1; PID:g780133

Query Match 100.0%; Score 104; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 4.7e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MITRGSVHQNFAADFTFATG 20

Db 343 MITRGSVHQNFAADFTFATG 362

### RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAP-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C:Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, M.; Tomita, M.; Yokoyama, J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KAR1>

A:Cross-references: DDBJ:D67037; MID:g1644228; PIDN:BA11054.1; PID:g1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MATS>

F:76.200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.7%; Score 86; DB 2; Length 436;  
Best Local Similarity 75.0%; Pred. No. 6e-07;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADFTFATG 20  
||:|||||:|||||  
DB 341 MIAVKGSVHNFVDFTFATG 360

## RESULT 3

T32756  
hypothetical protein W03G9.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32756

R:Dante, M.; Keppler, D.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid W03G9.

A:Reference number: Z21220

A:Accession: T32756

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-384 <DAN>

A:Cross-references: EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN00019; CESP:W03G9.6

A:Experimental source: strain Bristol N2; clone W03G9

C:Genetics:

A:Gene: CESP:W03G9.6

A:Map position: 1

A:Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 55.8%; Score 58; DB 2; Length 384;  
Best Local Similarity 52.9%; Pred. No. 0.035;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADFTF 17  
||:|||||:|||||  
DB 304 LTLGSAVHQSFDTDFPF 320

## RESULT 4

T28936

hypothetical protein C52B9.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T28936

R:Nelson, J.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid C52B9.

A:Reference number: Z20545

A:Accession: T28936

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-476 <NLE>

A:Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN000028; CESP:C52B9.7

A:Experimental source: strain Bristol N2; clone C52B9

C:Genetics:

A:Gene: CESP:C52B9.7

A:Map position: X

A:Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 51.9%; Score 54; DB 2; Length 476;  
Best Local Similarity 56.2%; Pred. No. 0.22;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 ITIRGSVHQNFADFTF 17  
||:|||||:|||||  
DB 397 LTLGSAVHQSFDTDFPF 412

## RESULT 5

## T47290

hypothetical protein T14K23.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: T47290

R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner

Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24458

A:Accession: T47290

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <NYA>

A:Cross-references: EMBL:AL132909

A:Experimental source: cultivar Columbia; BAC clone T14K23

C:Genetics:

A:Map position: 3

A:Introns: 109/2; 137/1; 219/1; 331/1; 365/3; 492/2

A:Note: T14K23.30

Query Match 50.0%; Score 52; DB 2; Length 541;  
Best Local Similarity 44.4%; Pred. No. 0.57;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFADFTFATG 20  
||:|||||:|||||  
DB 453 TVKGVHESFRDAVFALG 470

## RESULT 6

T47377

hypothetical protein T5C2.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: T47377

R:Obermaier, B.; Ottenwälder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke,

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24463

A:Accession: T47377

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-830 <OBE>

A:Cross-references: EMBL:AL138664

A:Experimental source: cultivar Columbia; BAC clone T5C2

C:Genetics:

A:Map position: 3

A:Introns: 52/3; 131/1; 171/2; 467/1; 552/1; 594/1; 710/1

A:Note: T5C2.50

Query Match 50.0%; Score 52; DB 2; Length 830;  
Best Local Similarity 50.0%; Pred. No. 0.92;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFADFTFATG 20  
||:|||||:|||||  
DB 57 TVKGVHESFRDAVFALG 74

## RESULT 7

T32949

hypothetical protein C05G6.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32949

R:Kemp, K.

submitted to the EMBL Data Library, February 1998

A:Description: The sequence of C. elegans cosmid C05G6.

A:Reference number: Z21252

A:Accession: T32949

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

Query Match 40.4%; Score 42; DB 2; Length 325;  
Best Local Similarity 53.8%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Yoon T : Khalak H  
K; Fasel, C.M.; NUT

Query Match 40.4%; Score 42; DB 2; Length 325;  
Best Local Similarity 53.8%; Pred. NO. 17;  
Matches 7: Conservative 2; Mismatches 4; Indels

They, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

A:Reference number: A71250; MUID:9832770

A:Accession: G71266

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1239 <COL>

A:Cross-references: GB:AE001259; GB:AE000520; NID:g3323209; PIDN:AA065853.1; PID:g3323209

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0898

Query Match 40.4%; Score 42; DB 2; Length 1239;

Best Local Similarity 63.6%; Pred. No. 77;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 HQNFADFTFAT 19

|||:|:|

Db 1132 HQRFAEFSFLT 1142

RESULT 13

T15957

hypothetical protein F02E8.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Mar-2001

C:Accession: T15957

R:Miller, N.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of *C. elegans* cosmid F02E8.

A:Reference number: Z18436

A:Accession: T15957

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-142 <MIL>

A:Cross-references: EMBL:U53340; NID:g1255859; PID:g1255861; PIDN:AAA96207.1; GSPDB:GN00

A:Experimental source: strain Bristol N2; clone F02E8

C:Genetics:

A:Gene: CESP:F02E8.3

A:Map position: X

A:Introns: 29/3; 89/3

C:Superfamily: mouse clathrin-associated protein 19

Query Match

Best Local Similarity 39.4%; Score 41; DB 2; Length 142;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ITIRGSVHQNFADF 15

:|:|:|:|:

Db 39 VTVRDAKHTNFVEF 52

RESULT 14

H86786

hypothetical protein yndB [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)

C:Species: *Lactococcus lactis* subsp. *lactis*

C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001

C:Accession: H86786

R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mearns, K.; Weissbach, J.; Ehrlich

Genome Res. In press, 2001

A:Title: The complete genome sequence of the lactic acid bacterium.

A:Reference number: A86625

A:Accession: H86786

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <STO>

A:Cross-references: GB:AE005176; NID:g12724273; PIDN:AAK05394.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yndB

Query Match 39.4%; Score 41; DB 2; Length 249;

Best Local Similarity 42.1%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 2 ITIRGSVHQNFADFTFATG 20

|||:|:|:|:

Db 204 ITIEGGNHSGFGSYGFGK 222

RESULT 15

E71690

minor telcholic acids biosynthesis protein ggab (ggab) RP339 - *Rickettsia prowazekii*

C:Species: *Rickettsia prowazekii*

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Nov-2000

C:Accession: E71690

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Als

Nature 396, 133-140, 1998

A:Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria

A:Reference number: A71630; MUID:99039499

A:Accession: E71690

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-318 <AND>

A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14799.1; PID:g

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: ggab; RP339

C:Superfamily: *Neisseria meningitidis* glycosyl transferase A

Query Match

Best Local Similarity 39.4%; Score 41; DB 1; Length 318;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFAD 14

|||:|:|:|:

Db 243 MIMKSGSTHQFLSD 256

Search completed: March 9, 2002, 00:34:14

Job time: 325 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:38 ; Search time 30.16 Seconds  
(without alignments)  
24.314 Million cell updates/sec

Title: US-09-922-067-11

Perfect score: 104  
Sequence: 1 MITIRGSVHQNFADTFATG 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	441	1	PAFA_HUMAN
2	100	96.2	444	1	PAFA_CANFA
3	94	90.4	444	1	PAFA_BOVIN
4	86	82.7	436	1	PAFA_CANVO
5	83	79.8	422	1	PAFA_CHICK
6	61	58.7	392	1	PAF2_HUMAN
7	59	56.7	352	1	PAF2_BOVIN
8	59	56.7	440	1	PAFA_MOUSE
9	54	51.9	476	1	PAFA_CAEEL
10	42	40.4	142	1	A2S1_HUMAN
11	42	40.4	142	1	A2S1_MOUSE
12	41	39.4	458	1	YM77_YEAST
13	40	38.5	296	1	THTR_MOUSE
14	40	38.5	579	1	ILVB_SEIPL
15	40	38.5	918	1	YNE6_CAEEL
16	39.5	38.0	540	1	THI6_YEAST
17	39.5	38.0	672	1	ANK6_RAT
18	39	37.5	178	1	V449_HAEIN
19	39	37.5	438	1	SECY_METVA
20	39	37.5	466	1	HEMN_SYNY3
21	39	37.5	585	1	DCHE_YEAST
22	39	37.5	1216	1	YXP3_CAEEL
23	39	37.5	1239	1	V120_EBV
24	39	37.5	2201	1	TENA_HUMAN
25	39	37.5	3411	1	POLG_YEFV1
26	39	37.5	3411	1	POLG_YEFV2
27	38.5	37.0	475	1	GAPN_STRMU
28	38	36.5	184	1	YPS2_SYNP2
29	38	36.5	351	1	Y630_RICPR
30	38	36.5	382	1	YOF3_CAEEL
31	38	36.5	452	1	MURE_STAAU
32	38	36.5	731	1	DNLJ_ZYMMO
33	37	35.6	121	1	YGIW_HAEIN

34	37	35.6	244	1	T2E5_ECOLI
35	37	35.6	296	1	THTR_HUMAN
36	37	35.6	303	1	PPV_DROME
37	37	35.6	305	1	PP66_HUMAN
38	37	35.6	305	1	PPP6_RAT
39	37	35.6	325	1	ATP3_ARATH
40	37	35.6	385	1	FTSZ_HELPJ
41	37	35.6	385	1	FTSZ_HELPY
42	37	35.6	397	1	POR_CHLRE
43	37	35.6	405	1	YBKO_BACSU
44	37	35.6	412	1	AK_PSEAE
45	37	35.6	510	1	DDC_ACIBA

#### ALIGNMENTS

RESULT 1					
ID	PAFA_HUMAN	STANDARD;	PRT;	441	AA.
AC	Q13093; Q15692;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)				
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED				
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE				
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).				
GN	PLA2G7 OR PAFAH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.				
RC	TISSUE=Myeloid;				
RX	MEDLINE=95214779; PubMed=7700381;				
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,				
RA	Schlimp B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,				
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;				
RA	"Anti-inflammatory properties of a platelet-activating factor				
RT	acetylhydrolase.";				
RN	Nature 374:549-553(1995).				
[2]					
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
TISSUE=Lymphoma;					
MEDLINE=96197208; PubMed=8624782;					
Tew D.G., Southan C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,					
Moore K., Gloger I.S., Macphie C.H.;					
"Purification, properties, sequencing, and cloning of a lipoprotein-					
associated, serine-dependent phospholipase involved in the oxidative					
modification of low-density lipoproteins.";					
Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).					
[3]					
MUTAGENESIS.					
MEDLINE=96029630; PubMed=7592717;					
Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,					
Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,					
Gray P.W.;					
"Plasma platelet-activating factor acetylhydrolase is a secreted					
phospholipase A2 with a catalytic triad.";					
J. Biol. Chem. 270:25481-25487(1995).					
[4]					
VARIANT PHE-279.					
MEDLINE=96259525; PubMed=8675689;					
Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,					
Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,					
McIntyre T.M., Gray P.W., Prescott S.M.;					
"Platelet-activating factor acetylhydrolase deficiency. A missense					
mutation near the active site of an anti-inflammatory					
phospholipase.";					
J. Clin. Invest. 97:2784-2791(1996).					
[5]					

VARIANT PHE-279.  
 MEDLINE-98430412; PubMed-9759612;  
 Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,  
 Yoshimizu N., Fukushi K., Satoh K.;  
 "A mutation in plasma platelet-activating factor acetylhydrolase  
 (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not  
 for hypertension";  
 Thromb. Haemost. 80:372-375(1998).  
 -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 PHOSPHOLIPIDS.  
 -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 -1- TISSUE SPECIFICITY: PLASMA.  
 -1- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS  
 PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT  
 PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY  
 RESPONSES.  
 -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 -----  
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 -----  
 EMBL; U20157; AAC50126.1; -;  
 EMBL; U24577; AAB04170.1; -;  
 MIM; 601690; -;  
 InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 PROSITE; PS00120; LIPASE\_SER; 1.  
 Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 441 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 273 273 ACETYLHYDROLASE.  
 FT ACT\_SITE 296 296 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 351 351 CHARGE RELAY SYSTEM.  
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .).  
 FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE  
 PROTEIN).  
 FT FTIG-Var 004268.  
 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 S->A: LOSS OF ACTIVITY.  
 D->A: ALMOST NO ACTIVITY.  
 D->N: DIMINISHED ACTIVITY.  
 D->A: LOSS OF ACTIVITY.  
 D->N: LOSS OF ACTIVITY.  
 D->A: NO CHANGE IN ACTIVITY.  
 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.  
 H->A: LOSS OF ACTIVITY.  
 V -> A (IN REF. 2).  
 FT CONFLICT 379 379  
 FT SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

Query Match 100.0%; Score 104; DB 1; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MITIRGSHVHQNFADEFTFATG 20  
 ||||||||||||||||  
 Db 343 MITIRGSHVHQNFADEFTFATG 362

RESULT 2

PAFA\_CANFA STANDARD; PRT; 444 AA.  
 AC Q28262;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACVLYDROLASE) (LDL-ASSOCIATED  
 PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 ON NCBI\_TaxID=9615;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Plasma;  
 RA MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;  
 "Plasma platelet-activating factor acetylhydrolase is a secreted  
 phospholipase A2 with a catalytic triad";  
 J. Biol. Chem. 270:25481-25487(1995).  
 RL -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 PHOSPHOLIPIDS.  
 -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 -1- TISSUE SPECIFICITY: PLASMA.  
 -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
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 -----  
 EMBL; U34246; AAC48484.1; -;  
 InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 PROSITE; PS00120; LIPASE\_SER; 1.  
 Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 444 PLATELET-ACTIVATING FACTOR  
 FT ACT\_SITE 274 274 ACETYLHYDROLASE.  
 FT ACT\_SITE 297 297 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 444 AA; 50136 MW; 814EF0AE38B074AC CRC64;  
 Query Match 96.2%; Score 100; DB 1; Length 444;  
 Best Local Similarity 95.0%; Pred. No. 1.3e-09;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MITIRGSHVHQNFADEFTFATG 20  
 ||||||||||||||||  
 Db 344 MITIRGSHVHQNFADEFTTGTG 363  
 RESULT 3  
 ID PAFA\_BOVIN STANDARD; PRT; 444 AA.

Q28017;  
01-NOV-1997 (Rel. 35, Created)  
01-NOV-1997 (Rel. 35, Last sequence update)  
20-AUG-2001 (Rel. 40, Last annotation update)  
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
PLA2G7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spine;  
RX MEDLINE=96029630; PubMed=7592717;  
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.:  
RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
phospholipase A2 with a catalytic triad.";  
RL J. Biol. Chem. 270:25481-25487(1995).  
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC PHOSPHOLIPIDS.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: PLASMA.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U34247; AAC48483.1; .  
CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
DR InterPro: IPR000734; Lipase.  
DR PROSITE: PS00120; LIPASE\_SER; 1.  
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 444  
FT PLATELET-ACTIVATING FACTOR  
FT ACETYLHYDROLASE.  
FT ACT\_SITE 274 274  
FT ACT\_SITE 297 297  
FT ACT\_SITE 352 352  
FT ACT\_SITE 352 352  
FT CARBOHYD 60 60  
FT CARBOHYD 200 200  
FT CARBOHYD 424 424  
FT CARBOHYD 434 434  
FT CARBOHYD 434 434  
FT SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;  
Query Match 90.4%; Score 94; DB 1; Length 444;  
Best Local Similarity 94.7%; Pred. No. 1.4e-08;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 MITIRGSVHQNFADTFAT 19  
DB 344 MITIRGSVHQNFADTFAT 362  
RESULT 4  
PAPA\_CAVPO STANDARD; PRT; 436 AA.  
ID PAPA\_CAVPO

P70583;  
01-NOV-1997 (Rel. 35, Created)  
01-NOV-1997 (Rel. 35, Last sequence update)  
20-AUG-2001 (Rel. 40, Last annotation update)  
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
PLA2G7 OR PAFAH.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=Liver;  
RX MEDLINE=97103479; PubMed=8947850;  
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,  
RA Yokoyama K., Setaka M., Nohima S.:  
RT "Cloning, expression and characterization of plasma  
platelet-activating factor-acetylhydrolase from guinea pig.";  
RL J. Biochem. 120:838-844(1996).  
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC PHOSPHOLIPIDS.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: PLASMA.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
CC -----  
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CC -----  
CC EMBL: D67037; BAAL1054.1; .  
CC InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
DR InterPro: IPR000734; Lipase.  
DR PROSITE: PS00120; LIPASE\_SER; 1.  
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 436  
FT PLATELET-ACTIVATING FACTOR  
FT ACETYLHYDROLASE.  
FT ACT\_SITE 271 271  
FT ACT\_SITE 294 294  
FT ACT\_SITE 349 349  
FT ACT\_SITE 349 349  
FT CARBOHYD 76 76  
FT CARBOHYD 200 200  
FT CARBOHYD 324 324  
FT CARBOHYD 324 324  
FT SEQUENCE 436 AA; 49062 MW; C359D96E392FFE11 CRC64;  
Query Match 82.7%; Score 86; DB 1; Length 436;  
Best Local Similarity 75.0%; Pred. No. 3.2e-07;  
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 1 MITIRGSVHQNFADTFATG 20  
DB 341 MIAVKGSVHNFVDFTFATG 360  
RESULT 5  
PAPA\_CHICK STANDARD; PRT; 422 AA.  
ID PAPA\_CHICK  
AC Q90678;  
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)  
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED  
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE  
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).  
 GN PLA2G7.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=96029630; PubMed=7592717;  
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,  
 RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;  
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted  
 RT phospholipase A2 with a catalytic triad.";  
 RL J. Biol. Chem. 270:25481-25487(1995).  
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
 CC PHOSPHOLIPIDS.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: PLASMA.  
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
 CC -----  
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 CC -----  
 DR EMBL; U34278; AAC59717.1; -;  
 DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro; IPR000734; Lipase.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 422  
 FT PLATELET-ACTIVATING FACTOR  
 FT ACETYLHYDROLASE.  
 FT ACT\_SITE 266 266  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 289 289  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 345 345  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 331 331  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376E9141 CRC64;  
  
 Query Match 79.88; Score 83; DB 1; Length 422;  
 Best Local Similarity 75.06; Pred. No. 1e-06;  
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
 Oy 1 MITIRGSVHQNFADFTFATG 20  
 |||||:|||||:|||||:  
 Db 337 MITIKGSVHQSFDPDFTVSG 356  
  
 RESULT 6  
 PAF2\_HUMAN  
 ID PAF2\_HUMAN STANDARD; PRT; 392 AA.  
 AC Q99487; O15458;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC

DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).  
 GN PAF4H2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97115847; PubMed=8955149;  
 RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
 RA Aoki J., Hattori M., Arai H., Inoue K.;  
 RT "cDNA cloning and expression of intracellular platelet-activating  
 RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
 RT acetylhydrolase.";  
 RL J. Biol. Chem. 271:33032-33038(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.; SEQUENCE OF 1-5, AND MASS SPECTROMETRY.  
 RC TISSUE=Prostate;  
 RX MEDLINE=98161812; PubMed=9494101;  
 RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphee C.H.,  
 RA Moores K., Gloer I.S., Tew D.G.;  
 RT "Expression, purification and characterization of a human  
 RT serine-dependent phospholipase A2 with high specificity for oxidized  
 RT phospholipids and platelet activating factor.";  
 RL Biochem. J. 330:1309-1315(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=97364701; PubMed=9218411;  
 RA Staforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;  
 RT "Platelet-activating factor acetylhydrolases.";  
 RL J. Biol. Chem. 272:17895-17898(1997).  
 CC -!- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
 CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
 CC FUNCTION WITH THE PLASMA-TYPE ENZYME.  
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
 CC -!- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,  
 CC 3,4-DICHLOROSOCUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DPP) AND  
 CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT  
 CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO  
 CC AMYGDALA AND FRONTAL CORTEX.  
 CC -!- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.  
 CC -!- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; D87845; BAA13468.1; -;  
 DR EMBL; U89386; AAC39707.1; -;  
 DR MIM; 602344; -;  
 DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 DR InterPro; IPR000734; Lipase.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hydrolase; Lipid degradation.  
 FT ACT\_SITE 236 236  
 FT ACT\_SITE 259 259  
 FT ACT\_SITE 314 314  
 FT ACT\_SITE 314 314  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CONFLICT 212 212  
 FT L -> F (IN REF. 2).  
 SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;  
  
 Query Match 58.78; Score 61; DB 1; Length 392;  
 Best Local Similarity 55.08; Pred. No. 0.0054;  
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADFTFATG 20  
          ::: ::::: :: | | |  
Db 306 IITVLGSVHRQSOTDEAFVTG 32

RESULT	7
PAF2_BOVIN	
ID	PAF2_BOVIN STANDARD; PRT; 392 AA.
AC	P79106;
DC	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DDT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2 (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPAS GN PAFAH2.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Verte
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminan
OC	Bovidae; Bovinae; Bos.
NCBI_taxid	NCBI_taxid=9913;
[1]	
RN	SEQUENCE FROM N A . AND PARTIAL SEQUENCE.
RP	

RC TISSUE=Kidney;  
RX MEDLINE=97115847; PubMed=89455149;  
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,  
RZ Aoki J., Hattori M., Arai H., Inoue K.:  
RT "CDNA cloning and expression of intracellular platelet-activating  
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF  
RT acetylhydrolase.";   
RL J. Biol. Chem. 271:33032-33038(1996).  
RN [2]  
RP REVIEW:  
RX MEDLINE=97364701; PubMed=9218411;  
RA Stafford D.M., McInyre T.M., Zimmerman G.A., Prescott S.M.;  
RZ "Platelet-activating factor acetylhydrolases.";   
RT J. Biol. Chem. 272:17895-17898(1997).  
EL  
CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT  
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC  
CC FUNCTION WITH THE PLASMA-TYPE I ENZYME.  
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE  
CC H(2)O + 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT  
CC LOWER LEVELS IN OTHER TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.

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CC EMBL: D87559; BAAI3419.1; --  
DR InterPro: IPR000379; Est\_lip\_thioest\_actsite.  
DR InterPro: IPR000734; Lipase.  
DR PROSITE: PS00120; LIPASE\_SER; 1.  
KW Hydrolase; Lipid degradation.  
FT ACT\_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).  
SQ SEQUENCE 392 AA; 43865 MW; 1DEACA2ADF4ACEA8 CRC64;

Query Match 56.7%; Score 59; DB 1; Length 392;  
Best Local Similarity 50.0%; Pred. No. 0.012;  
Matches 10: Conservative 4; Mismatches 6; Indels

Qy 1 MITIRGSVHQNEADFTFATG 20  
:|:|:|:|:|:|

Db 306 IITVLGSHRSLTDFVAVAG 325

[illegible]

TISSUE-Spleen;  
MEDLINE=56029630; PubMed=7592717;  
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,  
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,  
RA Gray P.W.;  
RT "plasma platelet-activating factor acetylhydrolase is a secreted  
RT phospholipase A2 with a catalytic triad.";  
RL J. Biol. Chem. 270:25481-25487(1995).  
CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)  
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY  
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT  
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN  
CC PHOSPHOLIPIDS.  
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H2O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).  
CC  
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	ENBL; U34277; AAC52274.1; --
DR	MGD; MGI:1351327; Pla297.
DR	InterPro; IPR000379; Est_lip_thioest_actsite.
DR	InterPro; IPR000734; Lipase.
DR	PROSITE; PS00120; LIPASE_SER: 1.
KW	Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT	SIGNAL 1 21 BY SIMILARITY.
FT	CHAIN 22 440 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE.
FT	ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SII)
FT	ACT_SITE 295 295 CHARGE RELAY SYSTEM (BY SII)
FT	ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SII)
FT	CARBOYD 59 59 N-LINKED (GLCNAC..) (POI)
FT	CARBOYD 75 75 N-LINKED (GLCNAC..) (POI)
FT	CARBOYD 199 199 N-LINKED (GLCNAC..) (POI)
SO	SEQUENCE 440 AA; 49361 MW; C8ZA68AD42F482EB CRC64;

Query Match 56.7%; Score 59; DB 1; Length 440;  
Best Local Similarity 68.8%; Pred. No. 0.014;

QY 5 RGSVHQNFADFTFATG 20  
: | | | | | | | |

Db 346 QGLRHQNFDDFFVTG 361

## RESULT 9

PAFA\_CAEEL  
ID PAFA\_CAEEL STANDARD; PRT; 476 AA.  
AC Q22943;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE HOMOLOG (EC 3.1.1.47).  
GN C52B9.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RL Nelson J.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +  
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.  
CC -!- SIMILARITY: STRONG, WITH VERTEBRATES PLATELET-ACTIVATING FACTOR  
CC ACETYLHYDROLASE.  
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).

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EMBL; U64598; AK39216.1; -;  
DR WormPep; C52B9.7; CE06966.  
DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
DR PROSITE; PS00120; LIPASE\_SER; FALSE NEG.  
KW Hypothetical protein; Hydrolase; Lipid degradation.  
FT ACT\_SITE 326 326 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 404 404 CHARGE RELAY SYSTEM (BY SIMILARITY).  
SQ SEQUENCE 476 AA; 53974 MW; D61DF01F396371E9 CRC64;

Query Match 51.9%; Score 54; DB 1; Length 476;

Best Local Similarity 56.2%; Pred. No. 0.11; Mismatches 4; Indels 0; Gaps 0;

Matches 9; Conservative

QY 2 ITRGSHVQNFADFTF 17

Db 397 LTLGAVHQCFSDPPF 412

## RESULT 10

A2S1\_HUMAN  
ID A2S1\_HUMAN STANDARD; PRT; 142 AA.  
AC P33680;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CLATHRIN COAT ASSEMBLY PROTEIN AP17 (CLATHRIN COAT ASSOCIATED PROTEIN  
DE AP17) (PLASMA MEMBRANE ADAPTOR AP-2 17 KDA PROTEIN) (HA2 17 KDA  
DE SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN 2 SMALL CHAIN).  
GN AP2S1 OR CLAPS2 OR AP17.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

SEQUENCE FROM N.A.  
RP TISSUE=Kidney;  
RX MEDLINE=97193186; Pubmed=9040778;  
RA Winterpacht A., Ende S., Enklaar T., Fuhrly M., Zabel B.;  
RT "Human CLAPS2 encoding AP17, a small chain of the clathrin-associated  
RT protein complex: CDNA cloning and chromosomal assignment to 19q13.2--  
RT >q13.3".  
RL Cytogenet. Cell Genet. 75:132-135(1996).  
RN [2]

SEQUENCE FROM N.A.  
RX MEDLINE=98440366; Pubmed=9767099;  
RA Holzmann K., Poeltl A., Saueremann G.;  
RT "A novel spliced transcript of human CLAPS2 encoding a protein  
RT alternative to clathrin adaptor protein AP17".  
RL Gene 220:39-44(1998).  
CC -!- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN  
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN  
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF  
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.  
CC AP17 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.  
CC -!- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS A HETEROTETRAMER  
CC COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN  
CC (AP50) AND A SMALL CHAIN (AP17).  
CC -!- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE  
CC CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES SMALL SUBUNITS  
CC FAMILY.

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EMBL; X97074; CAA65782.1; -;  
DR EMBL; AJ010148; CAA09018.1; -;  
DR MIM; 602242; -;  
DR InterPro; IPR000804; Clat\_adaptor\_s.  
DR Pfam; PF01217; Clat\_adaptor\_s; 1.  
DR PROSITE; PS00989; CLAT-ADAPTOR\_S; 1.  
KW Coated pits.  
SQ SEQUENCE 142 AA; 17018 MW; CA38AF1EC72D9BF0 CRC64;

Query Match 40.4%; Score 42; DB 1; Length 142;

Best Local Similarity 40.0%; Pred. No. 3.2;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MITRGSHVQNFADPF 15

Db 38 VVTVRDAKHTNFVEF 52

## RESULT 11

A2S1\_MOUSE  
ID A2S1\_MOUSE STANDARD; PRT; 142 AA.  
AC Q00380; P97626; P70626;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CLATHRIN COAT ASSEMBLY PROTEIN AP17 (CLATHRIN COAT ASSOCIATED PROTEIN  
DE AP17) (PLASMA MEMBRANE ADAPTOR AP-2 17 KDA PROTEIN) (HA2 17 KDA  
DE SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN 2 SMALL CHAIN).  
GN AP2S1 OR CLAPS2 OR AP17.  
OS Mus musculus (Mouse), and  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090, 10116;  
RN [1]  
RP SEQUENCE FROM N.A.

RC SPECIES-Rat; TISSUE-Brain;  
RX MEDLINE-91250426; PubMed-2040623;  
RA Kirchhausen T., Davis A.C., Frucht S., O'Brine Greco B.,  
RA Payne G.S., Tubb B.;  
RT APl7 and APl9, the mammalian small chains of the clathrin-associated  
RT protein complexes show homology to Yapi7p, their putative homolog in  
RT yeast.\*;  
RL J. Biol. Chem. 266:11153-11157(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN-WISTAR KYOTO;  
RA Adams L.D., Weirny I., Schwarz S.M.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse;  
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,  
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,  
RA Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,  
RA Theising B., Wylie T., Lemon G., Soares B., Wilson R., Waterston R.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN  
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN  
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF  
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.  
CC APl7 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.  
CC -!- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS A HETEROTETRAMER  
CC COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN  
CC (AP50) AND A SMALL CHAIN (APl7).  
CC -!- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE  
CC CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES SMALL SUBUNITS  
CC FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M37194; AAA40742.1; -;  
DR EMBL; U75917; AAB46980.1; -;  
DR EMBL; AA277150; -; NOT\_ANNOTATED\_CDS.  
DR PIR; B40535; B40535.  
DR InterPro; IPR000804; Clat\_adaptor\_s.  
DR Pfam; PF01217; Clat\_adaptor\_s; 1.  
DR PROSITE; PS00989; CLAT\_ADAPTOR\_S; 1.  
KW Coated pits.  
FT CONFLICT 83 83 A -> G (IN REF. 2).  
FT CONFLICT 109 110 KV -> RF (IN REF. 2).  
FT CONFLICT 117 117 M -> I (IN REF. 2).  
FT CONFLICT 126 126 T -> R (IN REF. 2).  
SQ SEQUENCE 142 AA; 17018 MW; CA3FD868C65AEDF6 CRC64;  
  
Query Match 40.4%; Score 42; DB 1; Length 142;  
Best Local Similarity 40.0%; Pred. No. 3.2;  
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MITRGSVHQNFADP 15  
Db 38 VVTVRDAKHTNFVEF 52  
:::|:|:|:|  
  
RESULT 12  
YMW7 YEAST  
ID YMW7 YEAST PRT; 458 AA.  
AC 005031;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HYPOTHETICAL 50.5 KDA PROTEIN IN RNAI-RNT1 INTERGENIC REGION.  
GN YMR238W OR YMR959.20.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO YEAST YKL046C.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; Z49939; CAA90209.1; -;  
DR SGD; S0004851; YMR238W.  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 1 21 POTENTIAL.  
FT TRANSMEM 438 458 POTENTIAL.  
SQ SEQUENCE 458 AA; 50540 MW; 908D7E672333EC03 CRC64;  
  
Query Match 39.4%; Score 41; DB 1; Length 458;  
Best Local Similarity 53.8%; Pred. No. 17;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 IITRGSVHQNFAD 14  
Db 129 ITVMGAVERNFYD 141  
:::|:|:|:|  
  
RESULT 13  
ITPR MOUSE  
ID ITPR MOUSE STANDARD; PRT; 296 AA.  
AC P52196;  
DT 01-OCT-1995 (Rel. 34, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1) (RHODANESE).  
GN TST.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Liver;  
RX MEDLINE-96074596; PubMed-7488186;  
RA Dooley T.P., Nair S.K., Garcia R.E., Courtney B.C.;  
RT "Mouse rhodanese gene (Tst): cDNA cloning, sequencing, and  
RT recombinant protein expression.";  
RL Biochem. Biophys. Res. Commun. 216:1101-1109(1995).  
CC -!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
CC DETOXIFICATION.  
CC -!- CATALYTIC ACTIVITY: THIOSULFATE + CYANIDE = SULFITE + THIOCYANATE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.  
CC -!- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
CC -!- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.  
CC  
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CC EMBL: U35741; AAC52342.1; -  
DR HSP: P00586; IRHD.  
DR SWISS-2DPAGE; P52196; MOUSE.  
DR MGD; MGI:98852; Tst.  
DR InterPro: IPR001307; Rhodanese.  
DR InterPro: IPR001763; Rhodanese\_domain.  
DR Pfam; PF00581; Rhodanese; 2.  
DR SMART; SM00450; RHOD; 2.  
DR PROSITE; PS00380; RHODANESE\_1; 1.  
DR PROSITE; PS00683; RHODANESE\_2; 1.  
KW Transferase; Mitochondrion.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT DOMAIN 1 142 A DOMAIN.  
FT DOMAIN 143 158 HINGE.  
FT DOMAIN 159 236 B DOMAIN.  
FT ACT\_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY  
FT SIMILARITY).  
FT ACT\_SITE 247 247 BY SIMILARITY.  
FT ACT\_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING  
FT (BY SIMILARITY).  
FT ACT\_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING  
FT (BY SIMILARITY).  
SQ SEQUENCE 296 AA; 33334 MW; 82089D80F9AE55A CRC64;

Query Match 38.5%; Score 40; DB 1; Length 296;  
Best Local Similarity 52.9%; Pred. No. 16;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 IRGSVHONFADFTTATG 20  
||||: ||| |  
DB 204 IRGSVNNPFMDLTKDG 220

RESULT 14  
ILVB SPIPL STANDARD; PRT; 579 AA.  
ID ILVB SPIPL  
AC P27868;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE ACETOLACTATE SYNTHASE (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE) (ALS  
DE {FRAGMENT}).  
GN ILVY.  
OS Spirulina platensis.  
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.  
OX NCBI\_TaxID=1156;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92381487; PubMed=1512571;  
RA Milano A., de Rossi E., Zavarra E., Barbierato L., Ciferri O.,  
RA Riccardi G.;  
RT "Molecular characterization of the genes encoding acetohydroxy acid  
synthase in the cyanobacterium spirulina platensis.";  
RL J. Gen. Microbiol. 138:1399-1408(1992).  
CC -|- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) -> 2 PYRUVATE.  
CC -|- COFACTOR: THIAMINE PYRROPHOSPHATE, AND MAGNESIUM ION.  
CC -|- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.  
CC -|- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPST.  
CC -----  
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DR EMBL: M75907; AAA26595.1; -  
DR PIR: B44857; B44857.  
DR HSP: P06169; IYPD.  
DR InterPro: IPR000399; TPP\_enzyme.  
DR Pfam; PF00205; TPP\_enzymes; 1.  
DR PROSITE; PS00187; TPP\_ENZYMES; PARTIAL.  
KW Branched-chain amino acid biosynthesis; Flavoprotein; Lyase;  
KW Thiamine pyrophosphate.  
FT ACT\_SITE 61 61 BY SIMILARITY.  
FT NON\_TER 579 579  
SQ SEQUENCE 579 AA; 63440 MW; BC94FEA728A7889A CRC64;

Query Match 38.5%; Score 40; DB 1; Length 579;  
Best Local Similarity 37.5%; Pred. No. 33;  
Matches 9; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

QY 1 MITIRGSVHONFA---DFTTATG 20  
|: :|: :||| ||| |  
DB 270 MLGMHTAYANFAVMELDFVIAG 293

RESULT 15  
YNE6 CAEEL STANDARD; PRT; 918 AA.  
ID YNE6 CAEEL  
AC P30645;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 31, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE PROBABLE 3',5'-CYCLIC PHOSPHODIESTERASE R08D7.6 (EC 3.1.4.17).  
GN R08D7.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fultson L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Lalster N.,  
RA Lattelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RL Nature 368:32-38(1994).  
CC -|- CATALYTIC ACTIVITY: NUCLEOSIDE 3',5'-CYCLIC PHOSPHATE + H(2)O -  
CC NUCLEOSIDE 5'-PHOSPHATE.  
CC -|- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
CC FAMILY. STRONG, TO MAMMALIAN TYPE 6 GMP PHOSPHODIESTERASES.  
CC -----  
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CC EMBL: Z12017; CAA78052.1; -  
DR PIR: S24462; S24462.  
DR PIR: S41041; S41041.  
DR WormPep; R08D7.6; CE01047.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; HDC.  
DR InterPro; IPR002073; PDEase.  
DR



DR Pfam; PF01590; GAF; 1.  
 DR Pfam; PF00233; PDEase; 1.  
 DR PRINTS; PR00387; PDIESTERASE1.  
 DR SMART; SM00065; GAF; 1.  
 DR SMART; SM00471; Hdc; 1.  
 DR PROSITE; PS00126; PDEASE\_I; 1.  
 KW Hypothetical protein; Hydrolase; CGMP  
 SQ SEQUENCE 918 AA; 104238 MW; CA59910AF4CD6155 CRC64;

Query Match 38.5%; Score 40; DB 1; Length 918;  
 Best Local Similarity 87.5%; Pred. No. 56;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 10 QNFADTFE 17  
 |||||  
 Db 423 QNFADFSF 430

Search completed: March 9, 2002, 00:47:39  
 Job time: 800 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:55 ; Search time 94.88 Seconds  
(without alignments)  
30.833 Million cell updates/sec

Title: US-09-922-067-11

Perfect score: 104

Sequence: 1 MTTIRGSVHONFADTFATG 20

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL-17:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58	55.8	384	5	O44753
2	52	50.0	541	10	Q9M3G4
3	52	50.0	830	10	Q9M184
4	52	50.0	996	10	Q9C925
5	45	43.3	303	4	Q9UIG9
6	45	43.3	363	2	P94630
7	44	42.3	429	1	Q9HKS7
8	43	41.3	341	5	O45052
9	43	41.3	400	4	Q9C034
10	43	41.3	493	4	Q9C035
11	43	41.3	534	5	Q9CZFS
12	43	41.3	846	12	Q9YKS8
13	43	41.3	849	12	Q9YKR7
14	43	41.3	1669	10	Q9LW42
15	42.5	40.9	268	10	Q9F012
16	42.5	40.9	3396	5	Q9VM55
17	42	40.4	142	5	Q9VDC3
18	42	40.4	374	3	Q04033
19	42	40.4	515	10	O81639

20	42	40.4	1230	10	Q92061
21	42	40.4	1239	2	O83868
22	41	39.4	142	5	Q19123
23	41	39.4	249	2	Q9CG14
24	41	39.4	318	2	Q9ZDI9
25	41	39.4	367	2	P72900
26	40.5	38.9	554	12	Q98Y30
27	40	38.5	352	5	Q23345
28	40	38.5	379	11	Q64627
29	40	38.5	425	2	P73829
30	40	38.5	463	2	O07346
31	40	38.5	463	2	P73374
32	40	38.5	599	2	Q9CFJ5
33	40	38.5	753	10	Q9C7W5
34	40	38.5	767	2	O25395
35	40	38.5	767	2	Q92LFA
36	40	38.5	942	6	Q9BDV5
37	39.5	38.0	213	2	O86734
38	39.5	38.0	342	11	Q9D432
39	39.5	38.0	375	2	Q9F5P1
40	39.5	38.0	620	11	Q9DA68
41	39.5	38.0	777	5	O45373
42	39.5	38.0	920	3	Q02531
43	39.5	38.0	1172	5	Q9VLG4
44	39	37.5	199	2	Q9HYW8
45	39	37.5	201	2	Q9L0M1

## ALIGNMENTS

RESULT 1

O44753 ID O44753 PRELIMINARY: PRT: 384 AA.  
AC O44753;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE W03G9.6 PROTEIN.  
GN W03G9.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
[1]

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
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DR EMBL: AL138664; CAB81576.1; -.  
KW Hypothetical protein.  
SO SEQUENCE 830 AA; 93088 MW; F66022BE96ADCD2E CRC64;

Query Match 50.0%; Score 52; DB 10; Length 830;  
Best Local Similarity 50.0%; Pred. No. 1.4;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFADFTFATG 20  
::: |||: || |  
Db 57 TVKGVVHKSFDAVFALG 74

RESULT 4  
Q9C925 PRELIMINARY; PRT; 996 AA.  
Q9C925:  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HYPOTHETICAL 113.8 KDA PROTEIN.  
F14G24.23.  
GN  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_taxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RR STRAIN=CV. COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Duon P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Guntler J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.-J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana";  
RL Nature 408:816-820(2000).  
RE EMBL: AC019018; AAC52281.1; -.  
RW Hypothetical protein.  
SQ SEQUENCE 996 AA; 113815 MW; ABE74EB60E39HFF CRC64;

Query Match 50.0%; Score 52; DB 10; Length 996;  
Best Local Similarity 50.0%; Pred. No. 1.8;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFADFTFATG 20  
::: |||: || |  
Db 390 TVKGVVHKSFDAVFALG 407

RESULT 5  
Q9UIC9 PRELIMINARY; PRT; 303 AA.  
Q9UIC9:  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE SERINE/THREONINE PROTEIN PHOSPHATASE CATALYTIC SUBUNIT.  
GN  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_taxID=3702;  
RN [1]  
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RX MEDLINE=21016719; PubMed=11130712;  
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RW Hypothetical protein.  
SQ SEQUENCE 996 AA; 113815 MW; ABE74EB60E39HFF CRC64;

Query Match	43.3%	Score 45;	DB 2;	Length 363;
Best Local Similarity	57.1%	Pred. No. 9.5;		
Matches	8;	Conservative	3;	Mismatches 0; Gaps 0;
QY	5	RGSVHQNFADFTFA 18		
Db	94	RGTLVQNFRDEVA 107		
RESULT 7				
ID	Q9HKS7	PRELIMINARY;	PRT;	429 AA.
AC	Q9HKS7;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DR	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	PROBABLE ASPARAGINYL--TRNA SYNTHETASE.			
GN	TA0519.			
OS	Thermoplasma acidophilum.			
OC	Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaaceae;			
OC	Thermoplasma.			
OX	NCBI_TaxID=2303;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-DSM 1728.			
RX	MEDLINE=20479972; PubMed=11029001;			
RA	Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,			
RA	Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumgaertel W.;			
RT	"The genome sequence of the thermoacidophilic scavenger Thermoplasma			
RT	acidophilum.";			
RL	Nature 407:508-513(2000).			
RL	EMBL; AL445064; CAC11659.1;			
DR	InterPro: IPR002309; tRNA-synt_2.			
DR	InterPro: IPR002312; tRNA-synt_asp.			
DR	Pfam; PF00152; tRNA-synt_2; 1.			
DR	Pfam; PF01336; tRNA-anti; 1.			
DR	PRINTS; PR01042; TRNASYNTHASP.			
KW	Aminoacyl-tRNA synthetase; Complete proteome.			
SEQUENCE	429 AA; 49947 MW; 266B477FCC0C32B6 CRC64;			
Query Match	42.3%	Score 44;	DB 1;	Length 429;
Best Local Similarity	35.0%	Pred. No. 17;		
Matches	7;	Conservative	7;	Mismatches 0; Gaps 0;
QY	1	MITIRGSVHQNFADFTFA 20		
Db	129	VLKIRSTVIRSFADFFYENG 148		
		::    :: :     :		
RESULT 8				
ID	O45052	PRELIMINARY;	PRT;	341 AA.
AC	O45052;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DR	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	C05G6.3 PROTEIN.			
GN	C05G6.3.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
RN	NCBI_TaxID=6239;			
RN	[1]			

RC SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Hurlon J., Connell M., Copsey T., Cooper A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favella A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,  
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Welnscock L., Wilkinson-Sproat J., Wohlman P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Kemp K.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF045635; AAC02556.1; --  
 DR InterPro: IPR002035; VWFA.  
 DR Pfam: PF00092; vwa.1  
 DR PRINTS: PR00453; VWFADOMAIN.  
 DR PROSITE: PS02034; VWFA; 1.  
 DR SMART: SM00327; VWA; 1.  
 SQ SEQUENCE 341 AA; 37460 MW; 2FF07E14C5CCF5D4 CRC64;

Query Match 41.3%; Score 43; DB 5; Length 341;  
 Best Local Similarity 57.1%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 IRGSHVHONFADFTT 17  
 I I I I I I I I  
 Db 312 ISGDVHHFTTDTVF 325

RESULT 9  
 Q9C034 PRELIMINARY; PRT; 400 AA.  
 AC Q9C034;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE TRIPARTITE MOTIF PROTEIN TRIM5 ISOFORM BETA.  
 GN TRIM5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Raymond A., Meroni G.;  
 RT "Deciphering the function of the tripartite motif containing  
 RT proteins.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF220026; AAG53480.1; --  
 SQ SEQUENCE 400 AA; 46037 MW; E8AC7B014BF58488 CRC64;

Query Match 41.3%; Score 43; DB 4; Length 400;  
 Best Local Similarity 43.8%; Pred. No. 24;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 RGSVHONFADFTTATG 20  
 I I I I I I I I

Db 332 RGTRYQTFVFNCTG 347  
 RESULT 10  
 Q9C035 PRELIMINARY; PRT; 493 AA.  
 AC Q9C035;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE TRIPARTITE MOTIF PROTEIN TRIM5 ISOFORM ALPHA.  
 GN TRIM5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Raymond A., Meroni G.;  
 RT "Deciphering the function of the tripartite motif containing  
 RT proteins.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF220025; AAG53479.1; --  
 SQ SEQUENCE 493 AA; 56338 MW; 8E61AAFD508AF6C0 CRC64;

Query Match 41.3%; Score 43; DB 4; Length 493;  
 Best Local Similarity 43.8%; Pred. No. 31;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 RGSVHONFADFTTATG 20  
 I I I I I I I I  
 Db 332 RGTRYQTFVFNCTG 347

RESULT 11  
 Q9GZF5 PRELIMINARY; PRT; 534 AA.  
 AC Q9GZF5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE C18H7.1 PROTEIN.  
 GN C18H7.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Tin-Mollam A., Fronick W.;  
 RT "The sequence of C. elegans cosmid C18H7.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF067607; AAF98615.1; --  
 DR InterPro: IPR002035; VWFA.  
 DR Pfam: PF00092; vwa; 2.  
 DR SMART: SM00327; VWA; 2.  
 DR PROSITE: PS02034; VWFA; 2.  
 SQ SEQUENCE 534 AA; 59740 MW; E61DCA420962192E CRC64;

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Query Match          41.3%; Score 43; DB 5; Length 534;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 IIRGSVHONFADTF 17
Db 505 ISGDVHHFTDVTFF 518
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RESULT 12
QYKRS8 PRELIMINARY; PRT; 846 AA.
AC QYKRS8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENV.
DN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-96BW11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.,
RA Essex M.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RT "Molecular Cloning and Phylogenetic Analysis of Human Immunodeficiency
RT Botswana.";
RT J. Virol. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C-96BW11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110965; AAD17093.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
SQ SEQUENCE 846 AA; 96283 MW; AD196033D328ED3C CRC64;

Query Match          41.3%; Score 43; DB 12; Length 846;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IIRGSVHONFAD 14
Db 133 VTVDNTHQNFDT 145
      | | : | | | | |
      | | : | | | | |

RESULT 13
QYKRS7 PRELIMINARY; PRT; 849 AA.
AC QYKRS7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENV.
DN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-96BW11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.,
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110965; AAD17093.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
SQ SEQUENCE 846 AA; 96283 MW; AD196033D328ED3C CRC64;

Query Match          41.3%; Score 43; DB 12; Length 846;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IIRGSVHONFAD 14
Db 133 VTVDNTHQNFDT 145
      | | : | | | | |
      | | : | | | | |

RESULT 14
QYKRS8 PRELIMINARY; PRT; 1669 AA.
AC QYKRS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HELICASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kapeko T., Kato T., Asamizu E., Tabata S.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL; AB016878; BAB01023.1; -
SQ SEQUENCE 1669 AA; 191650 MW; F6F5C4F7DD8BD866 CRC64;

Query Match          41.3%; Score 43; DB 10; Length 1669;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 IIRGSVHONFADTFATG 20
Db 1101 TIEGVVHRTYRDACYALG 1118
      | | | | | | | |
      | | | | | | | |

RESULT 15
QYKRS8 PRELIMINARY; PRT; 268 AA.
AC QYKRS8;
DT 01-MAR-2001 (TREMBlrel. 15, Created)
DT 01-MAR-2001 (TREMBlrel. 15, Last sequence update)
DE ENV.
DN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-96BW11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Marlink R.,

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01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 LECTIN-RELATED PROTEIN PRECURSOR.  
 Citrus paradisii (Grapefruit).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 eurosids II; Sapindales; Rutaceae; Citrus.  
 NCBI\_TaxID=37636;  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MARSH; TISSUE=2-5 GRAM FRUIT YOUNG FLAVEDO;  
 RA Sinisterra X.H., Shatters R.G. Jr., McCollum T.G., Doostdar H.,  
 RA Mayer R.T.;  
 RT "Expression of lectin homolog in grapefruit flavedo.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBAJ databases.  
 DR EMBL; AF283537; AAG38522.1; -;  
 DR InterPro; IPR000985; Lectin\_legA.  
 DR InterPro; IPR001220; Lectin\_legB.  
 DR Pfam; PF00138; lectin\_legA; 1.  
 DR PROSITE; PS00307; LECTIN\_LEGUME\_BETA; UNKNOWN.1.  
 SQ SEQUENCE 268 AA; 29147 MW; 0353BCA4896A9F27 CRC64;

Query Match 40.9%; Score 42.5; DB 10; Length 268;  
 Best Local Similarity 44.0%; Pred. No. 19;  
 Matches 11; Conservative 3; Mismatches 4; Indels 7; Gaps 1;  
 QY 2 ITIRGSVHONFAD-----FTFAT 19  
 DB 89 ITIKIRHONYTDRAGDGMTIFAS 113

Search completed: March 9, 2002, 00:46:58  
 Job time: 834 sec